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GenCore version 4.5
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OM protein - protein search, using sw model

Run on:

August 6, 2001, 09:33:05 ; Search time 32.37 Seconds

(without alignments)

580.582 Million cell updates/sec

Title:

US-09-524-531a-15

Perfect score:

1637

Sequence:

1 MALRRPPRLCARLPDFL..... VNVIRTDEEGDFRKSSFVI 310

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Scored:

412676 seqs, 60623988 residues

Number of hits satisfying chosen parameters:

412676

Minimum DB seq length:

0

Maximum DB seq length:

200000000

Post-processing:

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_0601:*

1: /SIDS8/gcdata/geneseq/geneseq/AA1980.DAT: *
 2: /SIDS8/gcdata/geneseq/geneseq/AA1981.DAT: *
 3: /SIDS8/gcdata/geneseq/geneseq/AA1982.DAT: *
 4: /SIDS8/gcdata/geneseq/geneseq/AA1984.DAT: *
 5: /SIDS8/gcdata/geneseq/geneseq/AA1985.DAT: *
 6: /SIDS8/gcdata/geneseq/geneseq/AA1987.DAT: *
 7: /SIDS8/gcdata/geneseq/geneseq/AA1988.DAT: *
 8: /SIDS8/gcdata/geneseq/geneseq/AA1989.DAT: *
 9: /SIDS8/gcdata/geneseq/geneseq/AA1990.DAT: *
 10: /SIDS8/gcdata/geneseq/geneseq/AA1991.DAT: *
 11: /SIDS8/gcdata/geneseq/geneseq/AA1992.DAT: *
 12: /SIDS8/gcdata/geneseq/geneseq/AA1993.DAT: *
 13: /SIDS8/gcdata/geneseq/geneseq/AA1994.DAT: *
 14: /SIDS8/gcdata/geneseq/geneseq/AA1995.DAT: *
 15: /SIDS8/gcdata/geneseq/geneseq/AA1996.DAT: *
 16: /SIDS8/gcdata/geneseq/geneseq/AA1997.DAT: *
 17: /SIDS8/gcdata/geneseq/geneseq/AA1998.DAT: *
 18: /SIDS8/gcdata/geneseq/geneseq/AA1999.DAT: *
 19: /SIDS8/gcdata/geneseq/geneseq/AA2000.DAT: *
 20: /SIDS8/gcdata/geneseq/geneseq/AA2001.DAT: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description	RESULT	1
1	1637	100.0	310	21 AAB2726	Human confluency r	XX	AAB2726 standard; Protein: 310 AA.
2	1637	100.0	310	21 AAB33457	Human PRO1868 prot	XX	AC: AAB2726;
3	1637	100.0	310	21 AAY96735	PRO1868, an A33 an	XX	DT: 23-FEB-2001 (first entry)
4	1637	100.0	310	22 AAB80272	Human PRO1868 prot	XX	DE: Human confluency regulated adhesion molecule 1 #2.
5	1637	100.0	310	22 AAB80383	Secreted protein e	XX	XX: Immunoglobulin superfamily; Ig Sf; vascular adhesion molecule; inflammation; cancer; wound; angiogenesis; human; confluency regulated adhesion molecule 1; CRAM-1; JAM-2.
6	1637	100.0	310	22 AAB80408	Secreted protein e	XX	KW: Homo sapiens.
7	1637	100.0	310	22 AAB80409	Secreted protein e	XX	KW: PN: WO20053749-A2.
8	1637	100.0	311	21 AAB38333	Human secreted pro	XX	XX: 14-SEP-2000.
9	1637	100.0	311	21 AAB38384	Human secreted pro	XX	XX: PD: 13-MAR-2000; 2000WO-EP02219.
10	1637	100.0	311	21 AAB38384	Gene #13 associate	XX	PR: 11-MAR-1999; 99EP-0200746.
11	1637	100.0	339	22 AAB80431	DR: WPI: 2000-587436/55.	XX	DR: N-PSDB: AAA95306.

Human IGFAm-6 immuno
 Human secreted pro
 Human confluency r
 Murine confluency
 Secreted protein e
 Human Junctional a
 Human secreted pro
 Human confluency r
 Murine confluency
 Human PRO245 prote
 Human PRO245 prote
 Human angiogenesis
 Human 5' RSR secre
 Mouse Junctional a
 A33 related antige
 Human PRO245 prote
 Human A33 receptor
 Amino acid sequenc
 P11 antigen prote
 Human PRO301 antit
 Human PRO301 prote
 Human A33 receptor
 Human PRO301 prote
 Human PRO301 prote
 Skin cell protein,

in the isolation of human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB3347 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention.

```
Query Match 100.0%; Score 1637; DB 21; Length 310;
Best Local Similarity 100.0%; Pred. No. 1. 2e-133;
Matches 310; Conservative 0; Mismatches 0; Indels 0;
```

Gaps 0;

1

10

Mod I

0036102

-A2.

299

sein kind

CASE II

phosphorus

Ylation

site"

QY 241 NIGGIGGVILWAVLALITIGICCAVRGGFINNKQDGESYKNGKPDGVNVRTDEEG 300
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 241 niggiggyvlwavlalitigiccavrgrgyfinnkqdgesykngkpdgvnirtydeeg 300
 CC diabetes and retinal disorders such as retinitis pigmentosa.
 CC The PRO nucleic acids have applications in molecular biology, including
 CC use as hybridization probes, and in chromosome and gene mapping.
 XX

RESULT 4
 AAB80272

ID AAB80272 standard; Protein; 310 AA.

XX

AC AAB80272;

XX

DT 24-APR-2001 (first entry)

XX

DE Human PRO1868 protein.

XX

KW human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;

KW antiparkinsonian; nootropic; neuroprotective; vulnerary; cardiant;

KW antiangiogenic; vasoactive; antiasthmatic; antirheumatic; cancer;

KW antiarthritic; antiinflammatory; antiidiabetic; antiviral; diabetes;

KW ophthalmological; gene therapy; skin disease; gastrointestinal disorder;

KW ischaemia; inflammation.

XX

OS Homo sapiens.

XX

WO200104311-A1.

XX

18-JAN-2001.

XX

PD 22-FEB-2000; 2000WO-US04414.

XX

PR 07-JUL-1999; 99US-0143048.

XX

PR 26-JUL-1999; 99US-015698.

XX

PR 28-JUL-1999; 99US-0146222.

XX

PR 08-SEP-1999; 99WO-US20594.

XX

PR 13-SEP-1999; 99WO-US20944.

XX

PR 15-SEP-1999; 99WO-US21090.

XX

PR 15-SEP-1999; 99WO-US21547.

XX

PR 05-OCT-1999; 99WO-US22089.

XX

PR 29-NOV-1999; 99WO-US28214.

XX

PR 16-DEC-1999; 99WO-US30095.

XX

PR 20-DEC-1999; 99WO-US30911.

XX

PR 0-DEC-1999; 99WO-US30999.

XX

PR 5-JAN-2000; 99WO-US00219.

XX

PA (GETH) GENENTECH INC.

XX

PI shkenazi AJ, Botstein D, Desnoyers L, Eaton DU, Ferrara N;

PI Filvaroff E, Fong S, Gao W, Gerber R, Gerritsen ME, Goddard A;

PI Godowski PJ, Grimaldi CJ, Gurney AL, Hiltan KJ, KJavin IJ;

PI Matier JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;

PI Williams PM, Wood WI;

XX

WPI: 2001-081051/09.

XX

DR N-PSDB; AAF72433.

XX

PT Sixty one nucleic acids encoding PRO polypeptides which are useful in

PT the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung

PT squamous cell carcinoma) and neurodegenerative diseases (e.g.

PT Alzheimer's disease).

XX

PS Claim 1; Fig 124; 393pp; English.

XX

CC The present sequence is one of sixty one novel secreted and

CC transmembrane PRO polypeptides. The PRO polypeptides are

CC useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung

CC squamous cell carcinoma), gastrointestinal disorders (e.g. enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease,

CC Parkinson's disease), wound repair, cardiovascular disorders (e.g. CC endometrial bleeding, angiogenesis, ischaemia such as coronary CC ischaemia, atherosclerosis), inflammatory disorders (e.g. asthma, CC rheumatoid arthritis, multiple sclerosis), infertility, AIDS and CC diabetes and retinal disorders such as retinitis pigmentosa. The PRO nucleic acids have applications in molecular biology, including CC use as hybridization probes, and in chromosome and gene mapping. CC Sequence 310 AA;

RESULT 5
 AAB80383

ID AAB80383 standard; protein; 310 AA.

XX

AC AAB80383;

XX

DT 24-APR-2001 (first entry)

XX

DE Secreted protein encoded by gene #13.

XX

KW Secreted protein; human; autoimmune; hyperproliferation;

KW cardiovascular; cerebrovascular; infection; food.

XX

OS Homo sapiens.

XX

WPI: 200107459-A1.

XX

01-FEB-2001.

XX

PR 20-JUL-2000; 2000WO-US19735.

XX

PR 23-JUL-1999; 99US-0145220.

XX

(HUMA-) HUMAN GENOME SCI INC.

XX

PT Rosen CA, Ruben SM, Ebner R, Duan RD, Ni J, Soppet DR, Moore PA;

PT Shi Y, Lafleur DW, Olsen HS, Birsie CB, Komatsoulis GA;

XX

WPI: 2001-123261/13.

XX

New isolated nucleic acid encoding 29 secreted proteins, for

PT diagnosing, preventing and treating e.g. autoimmune,

PT hyperproliferative, cardiovascular, and ocular diseases or disorders

PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM, Ebner R, Duan RD, Ni J, Soppet DR, Moore PA;
PI Shi Y, Lafleur DW, Olsen HS, Birse CE, Komatsoulis GA;
XX
DR WPI; 2001-123261/13.
XX
PT New isolated nucleic acid encoding 29 secreted proteins, for
PT diagnosing, preventing and treating e.g. autoimmune,
PT hyperproliferative, cardiovascular, and ocular diseases or disorders
PT and microorganism infections
XX
PS Claim 11; Page 559-560; 601pp; English.
XX
CC The present invention relates to 29 human secreted proteins. The
CC invention is used to prevent autoimmune diseases e.g. rheumatoid
CC arthritis, hyperproliferative disorders e.g. neoplasms of the
CC breast or liver, cardiovascular disorders e.g. cardiac arrest,
CC cerebrovascular disorders e.g. cerebral ischemia, angiogenesis,
CC nervous system disorders e.g. Alzheimer's disease, infections
CC caused by bacteria, viruses and fungi and ocular disorders e.g.
CC corneal infection. Also used in food preparations.
XX
SQ sequence 310 AA;
Query Match 100.0%; Score 1637; DB 22; Length 310;
Best Local Similarity 100.0%; **Pred.** No. 1.2e-133; **Matches** 310; **Conservative** 0; **Mismatches** 0; **Indels** 0; **Gaps** 0;
QY 1 MALRPPRPLRICARIPDFEFLFLFRGCLIGAVNLKSSNRTPWVDFESVLSCLTDSQ 60
Db 1 malrpprplrcaripdfefllfrgcligavnkksnrtppwvdfesvlscltdsq 60
QY 61 SDPRIEWKKIODEQTYVFENDKIQGDLAGRAEIGKTSLIKWNTRROSALYCEVAR 120
Db 61 sdpriewkkidqeqtyvfndkikgdlagraelgktslikwntrrdsalycevar 120
QY 121 NDRKEIDEIVELTYVKPVTPVCRVPAVPGKAVLHQSEGHPRPHYSWVNDVPL 180
Db 121 ndrkeideiveltvqkpvtpcrvpaavpgkavlhqseghprphyswvndvpl 180
QY 181 PTDSSRANPRENNSFHLSSEGTLVFTAVKHDSSOYCYIASNDAGSARCEQEMEVYL 240
Db 181 pdssranprfnssfhlnsetgtlftavkhdssqycciasndagsarceeqemevyl 240
QY 241 NIGGITGGVLVFLAVLALITLGICCAVRYGYFINNKQDGTSYKNGKPDGVNYRTDEEG 300
Db 241 niggigggvflavlalitlgiccaayrrgyfinkkqdgessyknpgkpdgnyirtdeeg 300
QY 301 DFRHKSSFVI 310
Db 301 dfrhkssfvi 310
SO sequence 311 AA;
Query Match 100.0%; Score 1637; DB 21; Length 311;
Best Local Similarity 100.0%; **Pred.** No. 1.2e-133; **Matches** 310; **Conservative** 0; **Mismatches** 0; **Indels** 0; **Gaps** 0;
QY 1 MALRPPRPLRICARIPDFEFLFLFRGCLIGAVNLKSSNRTPWVDFESVLSCLTDSQ 60
Db 1 malrpprplrcaripdfefllfrgcligavnkksnrtppwvdfesvlscltdsq 60
QY 61 SDPRIEWKKIODEQTYVFENDKIQGDLAGRAEIGKTSLIKWNTRROSALYCEVAR 120
Db 61 sdpriewkkidqeqtyvfndkikgdlagraelgktslikwntrrdsalycevar 120
QY 121 NDRKEIDEIVELTYVKPVTPVCRVPAVPGKAVLHQSEGHPRPHYSWVNDVPL 180
Db 121 ndrkeideiveltvqkpvtpcrvpaavpgkavlhqseghprphyswvndvpl 180
QY 181 PTDSSRANPRENNSFHLSSEGTLVFTAVKHDSSOYCYIASNDAGSARCEQEMEVYL 240
Db 181 pdssranprfnssfhlnsetgtlftavkhdssqycciasndagsarceeqemevyl 240
QY 241 NIGGITGGVLVFLAVLALITLGICCAVRYGYFINNKQDGTSYKNGKPDGVNYRTDEEG 300
Db 241 niggigggvflavlalitlgiccaayrrgyfinkkqdgessyknpgkpdgnyirtdeeg 300
Q6 Homo sapiens.
XX
PN WO200061623-A1.
RESULT 9
AAB30333 standard; Protein; 311 AA.
XX
AC AAB30333;
XX
DT 31-JAN-2001 (first entry)
XX
DE Human secreted protein encoded by gene 13 clone HAPS79.
XX
KW Immunosuppressive; antiarthritic; antirheumatic; antiproliferative;
KW cytotoxic; cardiotonic; vasotropics; cerebroprotective; neuroprotective;
KW nootropic; antibacterial; virucide; fungicide; ophthalmological; human;
XX
Homo sapiens.
XX
PN WO200061623-A1.
RESULT 9

XX	Sequence	311 AA;	CC	breast or liver, cardiovascular disorders e.g. cardiac arrest,	
SQ			CC	cerebrovascular disorders e.g. cerebral ischemia, angiogenesis,	
			CC	nervous system disorders e.g. Alzheimer's disease, infections	
			CC	caused by bacteria, viruses and fungi and ocular disorders e.g.	
			CC	corneal infection. Also used in food preparations.	
XX	Sequence	311 AA;	XX		
Query Match	100.0%	Score 1637; DB 21; Length 311;	Query Match	100.0%; Score 1637; DB 22; Length 339;	
Best Local Similarity	100.0%	Pred. No. 1.2e-133; Mismatches 0; Indels 0; Gaps 0;	Best Local Similarity	100.0%; Pred. No. 1.4e-133; Mismatches 0; Indels 0; Gaps 0;	
Matches	310; Conservative		Matches	310; Conservative	
PT	1	MALRAPPRLCARLPDFELLFRGCLIGAVNLUKSSNRTPVQEFESVELSCITDSQ	PT	1	MALRAPPRLCARLPDFELLFRGCLIGAVNLUKSSNRTPVQEFESVELSCITDSQ
PT	61	sdptiewkkiqdeqttyvifdknlgdlaigavnlksnrtppvqefesvelscitdsq	PT	61	sdptiewkkiqdeqttyvifdknlgdlaigavnlksnrtppvqefesvelscitdsq
Db	61	sdptiewkkiqdeqttyvifdknlgdlaigavnlksnrtppvqefesvelscitdsq	Db	61	sdptiewkkiqdeqttyvifdknlgdlaigavnlksnrtppvqefesvelscitdsq
Qy	121	NDRKEIDEVIELVQVKPVTGCRVKAVPGMATHQCESQGHPRHYSWYRNDVPL	Qy	121	NDRKEIDEVIELVQVKPVTGCRVKAVPGMATHQCESQGHPRHYSWYRNDVPL
Db	121	ndrkeidevIELVQVKPVTGCRVKAVPGMATHQCESQGHPRHYSWYRNDVPL	Db	121	ndrkeidevIELVQVKPVTGCRVKAVPGMATHQCESQGHPRHYSWYRNDVPL
Qy	181	PTDSRANPRRNSSFHLSBTGTLYVFTAVHKDDSGQYCTASNDAGSARCEEQEMEVYL	Qy	181	PTDSRANPRRNSSFHLSBTGTLYVFTAVHKDDSGQYCTASNDAGSARCEEQEMEVYL
Db	181	ptdsranprfnssfhlnsetgtiiftavhkdssqgqycciasndagsarceeqemevyl	Db	181	ptdsranprfnssfhlnsetgtiiftavhkdssqgqycciasndagsarceeqemevyl
Qy	241	NIGGIGGVIVLAVLALITLGICCAVRYGFINKQDGESYKRGKPGGVNVTRTDEG	Qy	241	NIGGIGGVIVLAVLALITLGICCAVRYGFINKQDGESYKRGKPGGVNVTRTDEG
Db	241	niggiggvivlavlalitlgiccavyrgyfinkqdggesyknpgkpdgvyirtdeeg	Db	241	niggiggvivlavlalitlgiccavyrgyfinkqdggesyknpgkpdgvyirtdeeg
Qy	301	DFRHKSFVI	Qy	301	DFRHKSFVI
Db	301	dfrhksfvi	Db	301	dfrhksfvi
RESULT	11		RESULT	11	
ID	AAB80431		ID	AAB80431	
AC	AAB80431;		AC	AAB80431;	
XX			XX		
DT	24-APR-2001	(first entry)	DT	24-APR-2001	(first entry)
DE	Gene #13 associated peptide #1.		DE	Gene #13 associated peptide #1.	
XX			XX		
KW	Secreted protein; human; autoimmune; hyperproliferation;		KW	Secreted protein; human; autoimmune; hyperproliferation;	
KW	cardiovascular; cerebrovascular; infection; food.		KW	cardiovascular; cerebrovascular; infection; food.	
XX			XX		
OS	Homo sapiens.		OS	Homo sapiens.	
XX			XX		
PN	0200107459-A1.		PN	0200107459-A1.	
XX			XX		
PD	01-FEB-2001.		PD	01-FEB-2001.	
XX			XX		
PR	20-JUL-2000; 2000WO-US19735.		PR	20-JUL-2000; 2000WO-US19735.	
XX			XX		
PR	23-JUL-1999; 99US-0145220.		PR	23-JUL-1999; 99US-0145220.	
XX			XX		
PA	(HUMA-) HUMAN GENOME SCI INC.		PA	(HUMA-) HUMAN GENOME SCI INC.	
XX			XX		
PI	Rosen CA, Ruben SM, Ebner R, Duan RD, Ni J, Soppet DR, Moore PA;		PI	Rosen CA, Ruben SM, Ebner R, Duan RD, Ni J, Soppet DR, Moore PA;	
PI	Shi Y, Lafleur DW, Olsen HS, Burse CF, Komatsuolis GA;		PI	Shi Y, Lafleur DW, Olsen HS, Burse CF, Komatsuolis GA;	
XX			XX		
DR	WPI: 2001-123261/13.		DR	WPI: 2001-123261/13.	
XX			XX		
PT	New isolated nucleic acid encoding 29 secreted proteins, for		PT	New isolated nucleic acid encoding 29 secreted proteins, for	
PT	diagnosing, preventing and treating e.g. autoimmune, hyperproliferative, cardiovascular, and ocular diseases or disorders		PT	diagnosing, preventing and treating e.g. autoimmune, hyperproliferative, cardiovascular, and ocular diseases or disorders	
PT	and microorganism infections -		PT	and microorganism infections -	
PT	Disclosure; Page 75; 601PP; English.		PT	Disclosure; Page 75; 601PP; English.	
XX			XX		
CC	The present invention relates to 29 human secreted proteins. The invention is used to prevent autoimmune diseases e.g. rheumatoid		CC	The present invention relates to 29 human secreted proteins. The invention is used to prevent autoimmune diseases e.g. rheumatoid	
CC	arthritis, hyperproliferative disorders e.g. neoplasms of the		CC	arthritis, hyperproliferative disorders e.g. neoplasms of the	
PR	22-DBC-1998; 98US-0113635.		PR	22-DBC-1998; 98US-0113635.	
PR	WO200029593-A2.		PR	WO200029593-A2.	
XX			XX		
PD	25-MAY-2000.		PD	25-MAY-2000.	
XX			XX		
PF	19-NOV-1999; 99WO-US27566.		PF	19-NOV-1999; 99WO-US27566.	
XX			XX		
PR	19-NOV-1998; 99US-0113635.		PR	19-NOV-1998; 99US-0113635.	
PR	22-DBC-1998; 98US-0113635.		PR	22-DBC-1998; 98US-0113635.	

PR 07-APR-1999; 9905-01288194.

XX (INCY-) INCITE PHARM INC.

XX YUE H, Tang YT, Corley NC, Guegler KJ, Gorgone GA, Baughn MR;

XX Lu DAM, Lal P, Hillman JL, Yang J;

XX DR WPI; 2000-387795/33.

XX N-PSDB; AAA27386.

XX

PT Immunoglobulin superfamily proteins, the agonist and antagonist of the protein is useful for preventing and treating disorders associated with altered levels of the protein such as cancer, immune system disorders

PT

XX

PS Claim 1; Page 82-83; 105pp; English.

XX

PT The present sequence is the human immunoglobulin superfamily protein C1QFAM-6. Its gene was isolated from a cDNA library of leg tissue. It is expressed in reproductive, nervous and cardiovascular tissue, where cancer and inflammation are common. The gene, protein, its antibodies, agonists and antagonists are suitable for diagnosing and treating many diseases, including cancer, immune system disorders (such as inflammation, AIDS, allergies, anaemia, arteriosclerosis, asthma, atherosclerosis, cholecystitis, Crohn's disease, diabetes mellitus, emphysema, Graves' disease, hepatitis, multiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma, systemic lupus erythematosus and ulcerative colitis), complications of cancer, haemodialysis and extracorporeal circulation, trauma and haematopoietic cancer (such as leukaemia) and infections caused by bacteria, viruses, fungi or parasites.

XX

SQ Sequence 310 AA:

Query Match 99.5%; Score 1629; DB 21; Length 310; Best Local Similarity 99.7%; Pred. No. 6.1e-13; Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 MALRRPPLRICALPDEFFLLFRGGLIGAVNLKSSNRTPWQEFSEVELSCIIDSQ 60

Db 1 malrprplrlcarlpdpffllfrgglgavnlksnprtvpqefsevelscildsq 60

Oy 61 SDPRIEKKIDQEQTYVFFDKIKQDLAGRAEILSTKSLKTIWNVRDSDALYCEVAR 120

D 61 sdpriekkiqeqttypfrdkikqgqlagraigletsklkwnvtrrdsalrycevar 120

Oy 121 NDRKEIDEIVELTVQKPVIPVCRPKAVPGKMATLHQSEGEHRRPHSWYRNVDPL 180

D 121 ndrkeideiveltvqkpvtpvcrpkavpgkmatlhcqeseqphprphswyrndpl 180

Oy 181 PTDSRANPRFRNSSFHINSETGTLVFAVKHDQSGOYCCIASNDAGSARCEQEMEYDD 240

Oy 181 ptdsransprfrnsfshinsetgtlvftavkhddsgqyyciasndagsarceeqemeydl 240

Oy 241 NIGGIGGVVLYLAVLILITLGICCAVRRGFINNIQDGESKNPKRPGNYIRDEEG 300

Db 241 niggiggvvlylavliitlgiccaavrgrgfinnkqdgeseqkpkpdgnyirtdeeg 300

Oy 301 DFRHKSFV 310

Db 301 dfrhksfv 310

XX

PS Sequence 285 AA:

Query Match 91.5%; Score 1498; DB 21; Length 285; Best Local Similarity 99.3%; Pred. No. 1.1e-12; Matches 283; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 26 GCLIGAVNLKSSNRTPWQEFSEVELSCIIDSQSDPRIEKKIDQEQTYVFFDKIKQ 85

Db 1 gcligavnlksnprtvpqefsevelscildsqsdpriekkiqeqttypfrdkikq 60

Oy 86 GDLAGRAEILGKSLKTIWNVRDSDALYCEVARNDRKEIDEIVELTVQKPVTPVCR 145

Db 61 gdlagraigletsklkwnvtrrdsalrycevarndrkideiveltvqkpvtpcr 120

Oy 146 VPKAVPGKMATLHQSEGEHRRPHSWYRNVDPLPSRANPRFRNSSFHINSETGTLV 205

Db 121 vpkavpgkmatlhcqeseqphprphswyrndplpsrancprfrnsfhsinsetgl 180

XX

DE Human secreted protein sequence encoded by gene 15 SEQ ID NO:134.

RESULT 13

AAB39254 standard; Protein: 285 AA.

ID AAB39254

AC AAB39254;

XX

XX 02-FEB-2001 (first entry)

RESULT 14
AAB27272
ID AAB27272 standard; Protein; 310 AA.
XX
AC AAB27272;
XX
DT 23-FEB-2001 (first entry)
XX
DE Human confluency regulated adhesion molecule 1 #1.
XX
KW Immunoglobulin superfamily; Ig Sf; vascular adhesion molecule;
KW inflammation; cancer; wound; angiogenesis; human;
KW confluency regulated adhesion molecule 1; CRAM-1; JAM-2.
OS Homo sapiens.
XX
PN WO200053749-A2.
XX
PD 14-SEP-2000.
XX
PP 13-MAR-2000; 2000WO-EP02219.
XX
PR 11-MAR-1999; 99EP-0200746.
XX
PA (RMFD-) RMF DICTAGENE SA.
XX
PI Imhof BA, Aurrand-Lions M;
XX
DR WPI; 2000-587436/55.
XX
PT Isolated human Confluency Regulated Adhesion Molecule 1 or 2 (CRAM-1 or
PT CRAM-2) polypeptide, useful for treatment of tumors, inflammation
XX
PS Claim 1; Fig 3; 59pp; English.

CC The present sequence is the human confluency regulated adhesion molecule
CC (CRAM-1, also known as JAM-2). CRAM-1 is one of the vascular adhesion
CC proteins of the immunoglobulin superfamily (Ig Sf). The CRAM-1 protein
CC and coding sequence can be used in the treatment of cancer, inflammation,
CC in the modulation of cell-cell interactions and angiogenesis, and
XX sequence 310 AA;

Query Match 86.1%; Score 1409; DB 21; Length 310;
Best Local Similarity 85.8%; Pred. No. 6.3e-114;
Matches 266; Conservative 18; Mismatches 26; Indels 0; Gaps 0;

QY 1 MALRPRPRLRICARAPDFEFLLEFLRGCLGAVNLKSSNRPVPPVDFESTELSCITDSOT 60
Db 1 malstrirrlyiariphfffillfrgcmleavnlnksnrrpvnviefesvclscithsq 60

QY 61 SDPRIEWKKTODEQTYVFENDKIOGDLAGRAEIGKTSUKIWNTRRDALYCEVAR 120
Db 61 sdpriewkkiqdgqttyvyrkqkdgldagrttdvfgtslriwntrsdaisyceval 120

QY 121 NDRKEIDEIVELTVQVKPVTPVCRVPKAVFVGKWAHLHQESECHPRPHYSWVRNDVPL 180
Db 121 ndrkeideielivqkpvtpvcriapaavpgkatalqcoesegyprphyswvndvpl 180

QY 181 PTDSRANPRFRNSSFHLNSEITGLVFTAVHKDDSQYCYIASNDGASARCEEQEMEVYD 240
Db 181 ptdsranprfrnssfhlNSEITGLVFTAVHKDDSQYCYIASNDGASARCEEQEMEVYD 240

RESULT 15
AAB27278
ID AAB27278 standard; Protein; 310 AA.
XX
AC AAB27278;
XX
DT 23-FEB-2001 (first entry)
XX
DE Murine confluency regulated adhesion molecule 1.
XX
KW Immunoglobulin superfamily; Ig Sf; vascular adhesion molecule;
KW confluency regulated adhesion molecule 1; CRAM-1; JAM-2.
OS Mus sp.
XX
PN WO200053749-A2.
XX
PD 14-SEP-2000.
XX
PP 13-MAR-2000; 2000WO-EP02219.
XX
PR 11-MAR-1999; 99EP-0200746.
XX
PA (RMFD-) RMF DICTAGENE SA.
XX
PI Imhof BA, Aurrand-Lions M;
XX
DR WPI; 2000-587436/55.
XX
PT N-PSDB; ARA97189.
XX
PT Isolated human Confluency Regulated Adhesion Molecule 1 or 2 (CRAM-1 or
PT CRAM-2) polypeptide, useful for treatment of tumors, inflammation
XX
PS Example; Fig 8; 59pp; English.

CC The present sequence is the murine confluency regulated adhesion molecule
CC 1 (CRAM-1, also known as JAM-2). CRAM-1 is one of the vascular adhesion
CC proteins of the immunoglobulin superfamily (Ig Sf). The CRAM-1 protein
CC and coding sequence can be used in the treatment of cancer, inflammation,
CC to modulate cell-cell interactions and angiogenesis, and in the
CC modulation of wound healing.

XX sequence 310 AA;

Query Match 86.1%; Score 1409; DB 21; Length 310;
Best Local Similarity 85.8%; Pred. No. 6.3e-114;
Matches 266; Conservative 18; Mismatches 26; Indels 0; Gaps 0;

QY 1 MALRPRPRLRICARAPDFEFLLEFLRGCLGAVNLKSSNRPVPPVDFESTELSCITDSOT 60
Db 1 malstrirrlyiariphfffillfrgcmleavnlnksnrrpvnviefesvclscithsq 60

QY 61 SDPRIEWKKTODEQTYVFENDKIOGDLAGRAEIGKTSUKIWNTRRDALYCEVAR 120
Db 61 sdpriewkkiqdgqttyvyrkqkdgldagrttdvfgtslriwntrsdaisyceval 120

QY 121 NDRKEIDEIVELTVQVKPVTPVCRVPKAVFVGKWAHLHQESECHPRPHYSWVRNDVPL 180
Db 121 ndrkeideielivqkpvtpvcriapaavpgkatalqcoesegyprphyswvndvpl 180

Db 121 ndrkeydeitielivqvkpvtptvcripaavpygkatalqceseyprphyswyndvpl 180
Qy 181 PTDSTRANPRFRNSSFHLNSEGTLLVTAHKDSDGQYCTASNDAGSARCEEQEMEVYDL 240
Db 181 ptdstranprfqnsffhvnsctglvfnahvhdsgqyctasndgaarceqgdmeydl 240
Qy 241 NGGGTGGVLVLAVALITKGICCAVRRGFINNIQDGESYKNRKPDPGNYIRIDEEG 300
Db 241 niagiiqgvivlivlavitmgicayrrgcfisskqdgeseyskspgkhgynyirtseeg 300
Qy 301 DFRHKSFFVI 310
Db 301 dfrhksffvi 310

Search completed: August 6, 2001, 09:33:06
Job time: 217 sec

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Human 5' EST secreted protein SEQ ID No. 294.
 Human; secreted protein; EST; expressed sequence tag; diagnosis; forensic; gene therapy; chromosome mapping; signal peptide; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haemopoiesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition.
Homo sapiens.
 WO9906551-A2.
 11-FEB-1999.
 31-JUL-1998; 98W01-TB01235.
 01-AUG-1997; 97W05-0905133.
 (GEST) GENSET.
 Ducleart A, Dumas Milne Edwards J, Lacroix B;
 WPI; 1999-153781/13.
 N-PSDB; AX39538.
 New nucleic acids encoding human secreted - proteins obtained from cDNA libraries prepared from substantia nigra, cerebellum, surrenals and fetal brain tissue

PT PT and fetal brain tissue
 XX CDNA libraries prepared from substantia nigra, cerebellum, surrenals
 XX
 PS Claim 34: Page 394: 434pp; English.
 CC AAX39440 to AAX39597 represent 5' expressed sequence tags (ESTs) for
 CC human secreted proteins, and encode the proteins given in AAY11374 to
 CC AAY11531, respectively. The proteins given represent the signal peptide
 CC and an N-terminal fragment of a secreted protein. The nucleic acid
 CC sequences can be used for producing secreted human gene products. They
 CC can also be used to develop products for diagnosis and therapy. The
 CC proteins obtained may have cytokine activity, cell
 CC proliferation/differentiation activity, haemopoiesis regulating
 CC activity, tissue growth regulating activity, reproductive hormone
 CC regulating activity, chemotactic/chemokinetic activity, haemostatic and
 CC thrombolytic activity, receptor/ligand activity, anti-inflammatory
 CC activity, tumour inhibition activity, or other activities. The products
 CC can be used in forensic, gene therapy and chromosome mapping procedures.
 CC The sequences can also be used for obtaining corresponding promoter
 CC sequences. The nucleic acids encoding the signal peptide can be used for
 CC directing extracellular secretion of a polypeptide or the insertion of a
 CC polypeptide into a membrane, or importing a polypeptide into a cell.
 XX
 Sequence 89 AA;
 SQ

ID AAY11472 standard; Protein; 89 AA.
 XX
 AC AAY11472;
 XX
 DT 21-JUN-1999 (first entry)

GenCore version 4.5
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OM protein - protein search, using sw model

Run on:

August 6, 2001, 09:34:17 ; Search time 25.41 Seconds

(without alignments)
929.324 Million cell updates/sec

Title: US-09-524-531A-15
Perfect score: 1637
Sequence: 1 MALRRPPRLICARLPDFL..... VNVIRTDEEGDFRKHSSFVI 310

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Scored: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 68.4
1: pir1;*
2: pir2;*
3: pir3;*
4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

RESULT	1	Score	Match	Length	DB ID	Description
	1	187	11.4	725	2 JE0099	neural cell adhesion molecule 1 - African clawed frog
	2	186	11.4	1088	1 IJXNL	neural cell adhesi
	3	180.5	11.0	1894	2 C54689	protein-tyrosine p
	4	177	10.8	725	2 JE0100	neural cell adhesi
	5	177	10.8	1092	1 JN0335	neural cell adhesi
	6	174	10.6	333	2 A1923	amalgam protein pr
	7	171.5	10.5	725	1 JMSNG	neural cell adhesi
	8	171.5	10.5	1115	1 JMSNL	neural cell adhesi
	9	169.5	10.4	1859	1 JRPNL	neural cell adhesi
	10	169.5	10.4	1912	2 A56178	protein-tyrosine-p
	11	164.5	10.0	3707	2 S18252	heparan sulfate pr
	12	163.5	10.0	1051	2 A39712	kinase-like protei
	13	161.5	9.9	853	1 IJBONC	neural cell adhesi
	14	161	9.8	538	2 T2457	vascular cell adhe
	15	161	9.8	1091	1 IJCINL	neural cell adhesi
	16	160.5	9.8	761	1 IJHNG	neural cell adhesi
	17	160.5	9.8	1612	2 T3005	dutul protein - mo
	18	159.5	9.7	7962	2 I38346	elastic titin - hu
	19	159.5	9.7	1033	2 S19247	cell adhesion prot
	20	159.5	9.7	6642	2 T29157	protein UNC-89 - C
	21	159	9.7	1323	2 PN0568	connectin 3B - chi
	22	159	9.7	4162	2 T42333	connectin/titin -
	23	157.5	9.5	1259	2 A43425	Bravo/Nr-CAM cell
	24	155.5	9.5	1268	1 A39460	neuronal cell adhesi
	25	155	9.5	344	2 I56551	neurotramin - rat
	26	155	9.5	1907	2 S5093	protein-tyrosine-p
	27	154.5	9.4	495	2 T57550	hypothetical prote
	28	154	9.4	1501	2 I58148	protein-tyrosine-p
	29	154	9.4	1863	2 S46217	protein-tyrosine-p

N:Alternate names: N-CAM 1
C:Species: Xenopus laevis (African clawed frog)
C:Date: 19-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C:Accession: JE0099
R:Kudo, M.; Takayama, E.; Tadakuma, T.; Shikawa, K.
Blochem. Biophys. Res. Commun. 245, 127-132, 1998
A:Title: Molecular cloning of ssd-form neural cell adhesion molecules (N-CAMS) as the
A:Reference number: JE0099; MUID:98204770
A:Accession: JE0099
A:Molecule type: mRNA
A:Residues: 1-725 <KUD>
A:Cross-references: DDbj:AB008162; NID:93116226; Pidn:BA25931.1; Pid:93116227
A:Experimental source: heart
C:Comment: This protein mediates and regulates various cell-cell interactions through
C:Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; 1
F:4132-475/Domain: immunoglobulin homology <IMM>
F:512-589/Domain: fibronectin type III repeat homology <3FR>
N:Alternate names: N-CAM 1
C:Species: Xenopus laevis (African clawed frog)
C:Accession: JE0099
R:Kudo, M.; Takayama, E.; Tadakuma, T.; Shikawa, K.
Blochem. Biophys. Res. Commun. 245, 127-132, 1998
A:Title: Molecular cloning of ssd-form neural cell adhesion molecules (N-CAMS) as the
A:Reference number: JE0099; MUID:98204770
A:Accession: JE0099
A:Molecule type: mRNA
A:Residues: 1-725 <KUD>
A:Cross-references: DDbj:AB008162; NID:93116226; Pidn:BA25931.1; Pid:93116227
A:Experimental source: heart
C:Comment: This protein mediates and regulates various cell-cell interactions through
C:Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; 1
F:4132-475/Domain: immunoglobulin homology <IMM>
F:512-589/Domain: fibronectin type III repeat homology <3FR>
N:Alternate names: N-CAM 1
C:Species: Xenopus laevis (African clawed frog)
C:Accession: JE0099
R:Krieg, P.A.; Sakaguchi, D.S.; Kintner, C.R.

Nucleic Acids Res. 17, 10321-10335, 1989
 A;Title: Primary structure and developmental expression of a large cytoplasmic domain from NCAM
 A;Reference number: S09600; MUID:90098871
 A;Accession: S09600
 A;Molecule type: mRNA
 A;Residues: 1-1088 <KTR>
 A;Cross-references: EMBL:W25596; NID:9214609; P10N:AAA49909 1; PID:9214610
 A;Note: the authors translated the codon AAA for residue 970 as Ieu
 C;Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM molecule
 C;Genetics: Several forms of NCAM are produced by alternative splicing.
 A;Gene: NCAM
 C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immunoglobulin superfamily; alternative splicing; brain; cell adhesion; duplication; heparin binding; signal sequence
 F;1-19/Domain: signal sequence #status predicted <SIG>
 F;20-1088/Product: neural cell adhesion molecule, long domain form #status predicted <LD>
 F;20-803/1050-1088/Product: neural cell adhesion molecule, short domain form #status predicted <SD>
 F;20-705/Domain: extracellular #status predicted <EXT>
 F;34-95/Domain: immunoglobulin homology <IMM2>
 F;153/Region: heparin binding #status predicted
 F;159-162/Region: heparin binding #status predicted
 F;381/Domain: immunoglobulin homology <IMM3>
 F;475/Domain: immunoglobulin homology <IMM5>
 F;512-589/Domain: fibronectin type III repeat homology <FN3A>
 F;618-679/Domain: fibronectin type III repeat homology <FN3B>
 F;705-723/Domain: transmembrane #status predicted <TM>
 F;724-1080/Domain: intracellular #status predicted <INT>
 F;2119-310,341,417,443,472/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;2119,310,341,417,443,472/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;1832/Binding site: substrate phosphate (Arg) #status predicted
 F;1832/Binding site: substrate phosphate (Arg) #status predicted
 Query Match 11.4%; Score 186; DB 1; Length 1088;
 Best Local Similarity 28.9%; Pred. No. 2.4e-07;
 Matches 61; Conservative 30; Mismatches 84; Indels 36; Gaps 11;
 Query Match 11.0%; Score 180.5; DB 2; Length 1894;
 Best Local Similarity 28.8%; Pred. No. 1.3e-07;
 Matches 72; Conservative 34; Mismatches 75; Indels 69; Gaps 15;
 Query Match 3 LRRPPRURL---CARLPDPFFLILFRGCLIGAVNLKSSNRPVQFEESVELSCIT 56
 Db 105 GTVNLIKUYKLTKEHAPTEGKEFEGDAVITCIVSSSISITWHKGK---VIFKK 159
 Query Match 57 DSQTSDPR-IEW---KKIODEQTYVFENDKIQGDLAGRTELGTSILKINWTRRDS 110
 Db 53 OA-TGDPRPKIVWNKKGGKVSQRFEVIED---GGSVLRQLR---TPRD 100
 Query Match 111 ALYCEVWNRDRKEDELYELTVQVKPVKPTVCPVCKAVPGKIN-----ATL 158
 Db 101 ALYEC---VASNNGEL-SVSIIRLTVRED---QIPRSEPTIDGPKLVVERTRATM 152
 Query Match 159 HQQESERGHPRPHYSWRYNDVPLPTDSRANPRFRNSSFHINSET-GTVFTAVHKDDSGQY 217
 Db 153 ICAAS-GNPDPPEITWFKDFLPVDT-SNNNGRK---QKRSIGALQLEOSEESESDQKY 206
 Query Match 218 YCIASNDAGS 227
 Db 207 ECVATNSAGT 216
 RESULT 3
 Query Match 10.8%; Score 177; DB 2; Length 725;
 Best Local Similarity 28.6%; Pred. No. 8.4e-07;
 Matches 60; Conservative 28; Mismatches 88; Indels 34; Gaps 10;
 Query Match 10.8%; Score 177; DB 2; Length 725;
 Best Local Similarity 28.6%; Pred. No. 8.4e-07;
 Matches 60; Conservative 28; Mismatches 88; Indels 34; Gaps 10;
 A;Title: MPTP delta, a putative murine homolog of HPTP delta, is expressed in specialized brain cells
 A;Reference number: A54689; MUID:93360986
 A;Accession: C54689
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-1894 <MI2>
 A;Experimental source: brain; splice form B
 A;Note: sequence inconsistent with nucleotide translation
 A;Note: sequence extracted from NCBI backbone (NCBIN:137486, NCBIPI:137487)

A;Accession: B54689
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-352, 'H', 354-535, 'S', 537-601, 1002-1894 <MI2>
 A;Experimental source: brain; splice form C
 A;Note: sequence inconsistent with nucleotide translation
 A;Note: sequence extracted from NCBI backbone (NCBIN:136527, NCBIPI:136530)
 C;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology
 C;Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester
 F;45-107/Domain: immunoglobulin homology <IMM1>
 F;245-299/Domain: immunoglobulin homology <IMM2>
 F;317-399/Domain: fibronectin type III repeat homology <FN2A>
 F;328-394/Domain: leukocyte common antigen cytosolic domain homology <LAC>
 F;165-184/Domain: protein-tirosine-phosphatase homology <PTP2>
 F;1536/Active site: Cys (phosphocysteine intermediate) #status predicted
 F;142-242/Binding site: substrate phosphate (Arg) #status predicted
 F;1826/Active site: Cys (phosphocysteine intermediate) #status predicted
 F;1832/Binding site: substrate phosphate (Arg) #status predicted
 Query Match 11.0%; Score 180.5; DB 2; Length 1894;
 Best Local Similarity 28.8%; Pred. No. 1.3e-07;
 Matches 72; Conservative 34; Mismatches 75; Indels 69; Gaps 15;
 Query Match 3 LRRPPRURL---CARLPDPFFLILFRGCLIGAVNLKSSNRPVQFEESVELSCIT 56
 Db 11 VWRPLSLLFTEFLCACAETPFRF-----TRPVPDQGIVSGCVAASFIC 52
 Query Match 57 DSQTSDPR-IEW---KKIODEQTYVFENDKIQGDLAGRTELGTSILKINWTRRDS 110
 Db 53 OA-TGDPRPKIVWNKKGGKVSQRFEVIED---GGSVLRQLR---TPRD 100
 Query Match 111 ALYCEVWNRDRKEDELYELTVQVKPVKPTVCPVCKAVPGKIN-----ATL 158
 Db 101 ALYEC---VASNNGEL-SVSIIRLTVRED---QIPRSEPTIDGPKLVVERTRATM 152
 Query Match 159 HQQESERGHPRPHYSWRYNDVPLPTDSRANPRFRNSSFHINSET-GTVFTAVHKDDSGQY 217
 Db 153 ICAAS-GNPDPPEITWFKDFLPVDT-SNNNGRK---QKRSIGALQLEOSEESESDQKY 206
 Query Match 218 YCIASNDAGS 227
 Db 207 ECVATNSAGT 216
 RESULT 4
 Query Match 10.8%; Score 177; DB 2; Length 725;
 Best Local Similarity 28.6%; Pred. No. 8.4e-07;
 Matches 60; Conservative 28; Mismatches 88; Indels 34; Gaps 10;
 Query Match 10.8%; Score 177; DB 2; Length 725;
 Best Local Similarity 28.6%; Pred. No. 8.4e-07;
 Matches 60; Conservative 28; Mismatches 88; Indels 34; Gaps 10;
 A;Title: Molecular cloning of ssd-form neural cell adhesion molecules (N-CAMS) as the
 A;Reference number: J00939; MUID:98204770
 A;Accession: JE0100
 A;Molecule type: mRNA
 A;Residues: 1-725 <KDR>
 A;Cross-references: DDBJ:AB008163; NID:93116228; P10N:BA25932.1; PID:93116229
 A;Experimental source: heart
 C;Comment: This protein mediates and regulates various cell-cell interactions through
 C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; 1.
 F;413-475/Domain: immunoglobulin homology <IMM>
 F;512-589/Domain: fibronectin type III repeat homology <3FR>

Scoring table:	BLOSUM62	93435 seqs, 3425486 residues	RESULT 1	VEJA_HUMAN	STANDARD;	PRT;	298 AA.
Searched:			ID	P57087_HUMAN			
Total number of hits satisfying chosen parameters:	93435		AC				
Minimum DB seq length: 0			DT	01-OCT-2000 (Rel. 4.0, Created)			
Maximum DB seq length: 2000000000			DT	01-OCT-2000 (Rel. 4.0, Last sequence update)			
Post-processing: Minimum Match 0%			DT	01-OCT-2000 (Rel. 4.0, Last annotation update)			
Post-processing: Maximum Match 100%			DE				
Database :	Swissprot_39;*		GN	C21ORF43.			
Scoring table:	BLOSUM62	Gapop 10.0 , Gapext 0.5	OS	Homo sapiens (Human).			
Searched:	93435 seqs, 3425486 residues		OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Total number of hits satisfying chosen parameters:	93435		OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo;			
Minimum DB seq length: 0			NCBI_TaxID=9606;				
Maximum DB seq length: 2000000000			RN				
Post-processing: Minimum Match 0%			RL	SEQUENCE FROM N A.			
Post-processing: Maximum Match 100%			RC	TISSUE=Vascular endothelial cells;			
Database :	Swissprot_39;*		RX	Medline=20317114; Published=1079521;			
Scoring table:	BLOSUM62	Gapop 10.0 , Gapext 0.5	RA	Palmeri D, van Zante A, Huang C C, Hemmerich S, Rosen S D ;			
Searched:	93435 seqs, 3425486 residues		RT	"Vascular endothelial junction-associated molecule, a novel member of the immunoglobulin superfamily, is localized to intercellular boundaries of endothelial cells."			
Total number of hits satisfying chosen parameters:	93435		RT	J. Biol. Chem. 275:19139-19145 (2000).			
Minimum DB seq length: 0			RL	-1 - FUNCTION MAY PLAY A ROLE IN THE PROCESSES OF LYMPHOCYTE HOMING TO SECONDARY LYMPHOID ORGANS.			
Maximum DB seq length: 2000000000			CC	-1 - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).			
Post-processing: Minimum Match 0%			CC	-1 - TISSUE SPECIFICITY: PROMINENTLY EXPRESSED ON HIGH ENDOTHELIAL VENULES BUT IS ALSO PRESENT ON THE ENDOTHELIA OF OTHER VESSELS.			
Post-processing: Maximum Match 100%			CC	LOCALIZED TO THE INTERCELLULAR BOUNDARIES OF HIGH ENDOTHELIAL CELLS.			
Database :	Swissprot_39;*		CC	-1 - SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.			
Scoring table:	BLOSUM62	Gapop 10.0 , Gapext 0.5	CC	-1 - SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.			
Searched:	93435 seqs, 3425486 residues		CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation in the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
Total number of hits satisfying chosen parameters:	93435		CC	CC			
Minimum DB seq length: 0			CC	CC			
Maximum DB seq length: 2000000000			CC	CC			
Post-processing: Minimum Match 0%			CC	CC			
Post-processing: Maximum Match 100%			CC	CC			
Database :	Swissprot_39;*		CC	CC			
Scoring table:	BLOSUM62	Gapop 10.0 , Gapext 0.5	CC	CC			
Searched:	93435 seqs, 3425486 residues		CC	CC			
Total number of hits satisfying chosen parameters:	93435		CC	CC			
Minimum DB seq length: 0			CC	CC			
Maximum DB seq length: 2000000000			CC	CC			
Post-processing: Minimum Match 0%			CC	CC			
Post-processing: Maximum Match 100%			CC	CC			
Database :	Swissprot_39;*		CC	CC			
Scoring table:	BLOSUM62	Gapop 10.0 , Gapext 0.5	CC	CC			
Searched:	93435 seqs, 3425486 residues		CC	CC			
Total number of hits satisfying chosen parameters:	93435		CC	CC			
Minimum DB seq length: 0			CC	CC			
Maximum DB seq length: 2000000000			CC	CC			
Post-processing: Minimum Match 0%			CC	CC			
Post-processing: Maximum Match 100%			CC	CC			
Database :	Swissprot_39;*		CC	CC			
Scoring table:	BLOSUM62	Gapop 10.0 , Gapext 0.5	CC	CC			
Searched:	93435 seqs, 3425486 residues		CC	CC			
Total number of hits satisfying chosen parameters:	93435		CC	CC			
Minimum DB seq length: 0			CC	CC			
Maximum DB seq length: 2000000000			CC	CC			
Post-processing: Minimum Match 0%			CC	CC			
Post-processing: Maximum Match 100%			CC	CC			
Database :	Swissprot_39;*		CC	CC			
Scoring table:	BLOSUM62	Gapop 10.0 , Gapext 0.5	CC	CC			
Searched:	93435 seqs, 3425486 residues		CC	CC			
Total number of hits satisfying chosen parameters:	93435		CC	CC			
Minimum DB seq length: 0			CC	CC			
Maximum DB seq length: 2000000000			CC	CC			
Post-processing: Minimum Match 0%			CC	CC			
Post-processing: Maximum Match 100%			CC	CC			
Database :	Swissprot_39;*		CC	CC			
Scoring table:	BLOSUM62	Gapop 10.0 , Gapext 0.5	CC	CC			
Searched:	93435 seqs, 3425486 residues		CC	CC			
Total number of hits satisfying chosen parameters:	93435		CC	CC			
Minimum DB seq length: 0			CC	CC			
Maximum DB seq length: 2000000000			CC	CC			
Post-processing: Minimum Match 0%			CC	CC			
Post-processing: Maximum Match 100%			CC	CC			
Database :	Swissprot_39;*		CC	CC			
Scoring table:	BLOSUM62	Gapop 10.0 , Gapext 0.5	CC	CC			
Searched:	93435 seqs, 3425486 residues		CC	CC			
Total number of hits satisfying chosen parameters:	93435		CC	CC			
Minimum DB seq length: 0			CC	CC			
Maximum DB seq length: 2000000000			CC	CC			
Post-processing: Minimum Match 0%			CC	CC			
Post-processing: Maximum Match 100%			CC	CC			
Database :	Swissprot_39;*		CC	CC			
Scoring table:	BLOSUM62	Gapop 10.0 , Gapext 0.5	CC	CC			
Searched:	93435 seqs, 3425486 residues		CC	CC			
Total number of hits satisfying chosen parameters:	93435		CC	CC			
Minimum DB seq length: 0			CC	CC			
Maximum DB seq length: 2000000000			CC	CC			
Post-processing: Minimum Match 0%			CC	CC			
Post-processing: Maximum Match 100%			CC	CC			
Database :	Swissprot_39;*		CC	CC			
Scoring table:	BLOSUM62	Gapop 10.0 , Gapext 0.5	CC	CC			
Searched:	93435 seqs, 3425486 residues		CC	CC			
Total number of hits satisfying chosen parameters:	93435		CC	CC			
Minimum DB seq length: 0			CC	CC			
Maximum DB seq length: 2000000000			CC	CC			
Post-processing: Minimum Match 0%			CC	CC			
Post-processing: Maximum Match 100%			CC	CC			
Database :	Swissprot_39;*		CC	CC			
Scoring table:	BLOSUM62	Gapop 10.0 , Gapext 0.5	CC	CC			
Searched:	93435 seqs, 3425486 residues		CC	CC			
Total number of hits satisfying chosen parameters:	93435		CC	CC			
Minimum DB seq length: 0			CC	CC			
Maximum DB seq length: 2000000000			CC	CC			
Post-processing: Minimum Match 0%			CC	CC			
Post-processing: Maximum Match 100%			CC	CC			
Database :	Swissprot_39;*		CC	CC			
Scoring table:	BLOSUM62	Gapop 10.0 , Gapext 0.5	CC	CC			
Searched:	93435 seqs, 3425486 residues		CC	CC			
Total number of hits satisfying chosen parameters:	93435		CC	CC			
Minimum DB seq length: 0			CC	CC			
Maximum DB seq length: 2000000000			CC	CC			
Post-processing: Minimum Match 0%			CC	CC			
Post-processing: Maximum Match 100%			CC	CC			
Database :	Swissprot_39;*		CC	CC			
Scoring table:	BLOSUM62	Gapop 10.0 , Gapext 0.5	CC	CC			
Searched:	93435 seqs, 3425486 residues		CC	CC			
Total number of hits satisfying chosen parameters:	93435		CC	CC			
Minimum DB seq length: 0			CC	CC			
Maximum DB seq length: 2000000000			CC	CC			
Post-processing: Minimum Match 0%			CC	CC			
Post-processing: Maximum Match 100%			CC	CC			
Database :	Swissprot_39;*		CC	CC			
Scoring table:	BLOSUM62	Gapop 10.0 , Gapext 0.5	CC	CC			
Searched:	93435 seqs, 3425486 residues		CC	CC			
Total number of hits satisfying chosen parameters:	93435		CC	CC			
Minimum DB seq length: 0			CC	CC			
Maximum DB seq length: 2000000000			CC	CC			
Post-processing: Minimum Match 0%			CC	CC			
Post-processing: Maximum Match 100%			CC	CC			
Database :	Swissprot_39;*		CC	CC			
Scoring table:	BLOSUM62	Gapop 10.0 , Gapext 0.5	CC	CC			
Searched:	93435 seqs, 3425486 residues		CC	CC			
Total number of hits satisfying chosen parameters:	93435		CC	CC			
Minimum DB seq length: 0			CC	CC			
Maximum DB seq length: 2000000000			CC	CC			
Post-processing: Minimum Match 0%			CC	CC			
Post-processing: Maximum Match 100%			CC	CC			
Database :	Swissprot_39;*		CC	CC			
Scoring table:	BLOSUM62	Gapop 10.0 , Gapext 0.5	CC	CC			
Searched:	93435 seqs, 3425486 residues		CC	CC			
Total number of hits satisfying chosen parameters:	93435		CC	CC			
Minimum DB seq length: 0			CC	CC			
Maximum DB seq length: 2000000000			CC	CC			
Post-processing: Minimum Match 0%			CC	CC			
Post-processing: Maximum Match 100%			CC	CC			
Database :	Swissprot_39;*		CC	CC			
Scoring table:	BLOSUM62	Gapop 10.0 , Gapext 0.5	CC	CC			
Searched:	93435 seqs, 3425486 residues		CC	CC			
Total number of hits satisfying chosen parameters:	93435		CC	CC			
Minimum DB seq length: 0			CC	CC			
Maximum DB seq length: 2000000000			CC	CC			
Post-processing: Minimum Match 0%			CC	CC			
Post-processing: Maximum Match 100%			CC	CC			
Database :	Swissprot_39;*		CC	CC			
Scoring table:	BLOSUM62	Gapop 10.0 , Gapext 0.5	CC	CC			
Searched:	93435 seqs, 3425486 residues		CC	CC			
Total number of hits satisfying chosen parameters:	93435		CC	CC			
Minimum DB seq length: 0			CC	CC			
Maximum DB seq length: 2000000000			CC	CC			
Post-processing: Minimum Match 0%			CC	CC			
Post-processing: Maximum Match 100%			CC	CC			
Database :	Swissprot_39;*		CC	CC			
Scoring table:	BLOSUM62	Gapop 10.0 , Gapext 0.5	CC	CC			
Searched:	93435 seqs, 3425486 residues		CC	CC			
Total number of hits satisfying chosen parameters:	93435		CC	CC			
Minimum DB seq length: 0			CC	CC			
Maximum DB seq length: 2000000000			CC	CC			
Post-processing: Minimum Match 0%			CC	CC			
Post-processing: Maximum Match 100%			CC	CC			
Database :	Swissprot_39;*		CC	CC			
Scoring table:	BLOSUM62	Gapop 10.0 , Gapext 0.5	CC	CC			
Searched:	93435 seqs, 3425486 residues		CC	CC			
Total number of hits satisfying chosen parameters:	93435		CC	CC			
Minimum DB seq length: 0			CC	CC			
Maximum DB seq length: 2000000000			CC	CC			
Post-processing: Minimum Match 0%			CC	CC			
Post-processing: Maximum Match 100%			CC	CC			
Database :	Swissprot_39;*		CC	CC			
Scoring table:	BLOSUM62	Gapop 10.0 , Gapext 0.5	CC	CC			
Searched:	93435 seqs, 3425486 residues		CC	CC			
Total number of hits satisfying chosen parameters:	93435		CC	CC			
Minimum DB seq length: 0			CC	CC			
Maximum DB seq length: 2000000000			CC	CC			
Post-processing: Minimum Match 0%			CC	CC			
Post-processing: Maximum Match 100%			CC	CC			
Database :	Swissprot_39;*		CC	CC			
Scoring table:	BLOSUM62	Gapop 10.0 , Gapext 0.5	CC	CC			
Searched:	93435 seqs, 3425486 residues		CC	CC			
Total number of hits satisfying chosen parameters:	93435		CC	CC			
Minimum DB seq length: 0			CC	CC			
Maximum DB seq length: 2000000000			CC	CC			
Post-processing: Minimum Match 0%			CC	CC			
Post-processing: Maximum Match 100%			CC	CC			
Database :	Swissprot_39;*		CC	CC			
Scoring table:	BLOSUM62	Gapop 10.0 , Gapext 0.5	CC	CC			
Searched:	93435 seqs, 3425486 residues		CC	CC			
Total number of hits satisfying chosen parameters:							

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OM protein - protein search, using sw model

Run on: August 6, 2001, 09:38:32 : Search time 35.5 Seconds
(without alignments)
1155.340 Million cell updates/sec

Title: US-09-524-531A-15

Perfect score: 1637

Sequence: 1 MALRRPPRLCARLPDFPL.....VNIRTDEEGDFRHKSFFV1 31.0

Scoring table: BLOSUM62

Gapext 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_16;*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_unclassified:*

13: sp_vertebrate:*

14: sp_virus:*

SPTREMBL_16;*

1155.340 Million cell updates/sec

Q9aj1 xenopus lae

Q9v3a5 drosophila

Q02870 gallus galli

Q29123 sus scrofa

Q9t180 canis famili

Q2826 hom sapien

Q9p121 homo sapien

Q9v444 drosophila

Q28939 sus scrofa

Q9aj1 xenopus lae

Q89026 mus musculu

Q9eq99 mus musculu

Q9eq88 mus musculu

Q10465 hom sapien

Q9ukv4 hom sapien

Q9j242 gallus galli

Q24327 drosophila

Q9v643 drosophila

Q01761 caenorhabdi

Q08476 gallus galli

Q9iaj0 xenopus lae

Q96918 gallus galli

Q57596 gallus galli

Q9dg15 gallus galli

Q9v895 drosophila

Q9hck4 hom sapien

ALIGNMENTS

RESULT 1
Q9EPK4 PRELIMINARY;
ID Q9EPK4
AC Q9PK4;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE JUNCTIONAL ADHESION MOLECULE-2, JAM-2.
GN JAM-2.
OS Mus musculus (Mouse).
EUkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.N.
RX PubMed=11036763;
RA Aurand-Lions M.A.; Duncan L.; Du Pasquier L.; Imhof B.A.;
"Cloning of JAM-2 and JAM-3: an Emerging Junctional Adhesion Molecular
Family?";
RL Curr. Top. Microbiol. Immunol. 251:91-98 (2000).
DR EMBL; AJ30034; CAC0041; -.
SQ SEQUENCE 310 AA; 34837 MW; 4B92BCB51D0A4B0A CRC64;

Query Match 86.9%; Score 1423; DB 11; Length 310;
Best Local Similarity 86.5%; Pred. No. 5.4e-129;
Matches 268; Conservative 18; Mismatches 24; Indels 0; Gaps 0;

QY 1 MALRRPPURCARLPDFFLLFRGCLIGAVNLKSSNRTPYVQEFESVELSCLITDSQT 60
Db 1 MALSRLRLRLYARLPDFFLLFRGCLIGRTVYFDNKIQGDQTWVYFDNKIQGDLAGTDFVGEKSLRLWNVTRSDSAIYRCVVAL 60

QY 61 SDPRIEKWIKQDQTTVYFDNKIQGDLAGTDFVGEKSLRLWNVTRSDSAIYRCVVAL 120
Db 61 SDPRIEKWIKQDQTTVYFDNKIQGDLAGTDFVGEKSLRLWNVTRSDSAIYRCVVAL 120

QY 121 NDRKEIDIVIEITVQVPTVCRVPAVPGTATLQCQSEGYPHYPHYSWYRNVDPL 180
Db 121 NDRKEIDIVIEITVQVPTVCRVPAVPGTATLQCQSEGYPHYPHYSWYRNVDPL 180

QY 181 PTDsRANPRFRNFSFHNLSETGTVQVPTVCRVPAVPGTATLQCQSEGYPHYPHYSWYRNVDPL 180
Db 181 PTDsRANPRFRNFSFHNLSETGTVQVPTVCRVPAVPGTATLQCQSEGYPHYPHYSWYRNVDPL 180

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1423	86.9	310	11 Q9EPK4	Q9epk4 mus musculu
2	486.5	29.7	298	11 Q9j159	Q9j159 mus musculu
3	463.5	28.3	300	11 Q9jhy1	Q9jhy1 rattus norv
4	336	20.5	259	4 Q9j3b2	Q9jkd5 rattus norv
5	326	19.9	273	11 Q9jrd5	Q91664 xenopus lae
6	242	14.8	318	13 Q9i664	Q9ix42 hom sapien
7	240.5	14.7	284	4 Q9rx42	Q97791 hom sapien
8	240.5	14.7	325	4 Q95791	Q9z109 mus musculu
9	233.5	14.3	328	11 Q9z109	Q9jka5 mus musculu
10	215.5	13.2	319	11 Q9jka5	Q9pwr4 gallus galli
11	206.5	12.6	335	13 Q9pwr4	Q9ygh1 gallus galli
12	203.5	12.4	335	13 Q9ygh1	Q91665 xenopus lae
13	203	12.4	181	13 Q91665	Q9ygv5 gallus galli
14	198.5	12.1	335	13 Q9ygv5	Q916b4 hom sapien
15	193.5	11.8	373	4 Q9hcb4	Q9490 hom sapien
16	189.5	11.6	358	4 Q9490	Q9532 hom sapien
17	188	11.5	259	4 Q9532	Q73633 xenopus lae
18	187	11.4	725	13 Q73633	Q64487 mus musculu
19	180.5	11.0	1894	11 Q64487	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	424	25.9	299	4	US-09-168-930-331
2	412	25.2	299	4	US-09-188-930-189
3	220	14.0	319	1	US-08-597-493B-22
4	169.5	10.4	390	2	US-08-919-424-1
5	160.5	9.8	365	4	US-08-928-383B-2
6	155.5	9.7	365	2	US-08-919-424-3
7	155.5	9.7	365	4	US-09-272-496-2
8	157.5	9.6	1101	3	US-08-386-485-2
9	155.5	9.5	612	2	US-08-152-30B-11
10	154	9.4	1501	2	US-08-447-464-3
11	154	9.4	1501	2	US-08-716-679-3
12	152.5	9.3	869	1	US-08-374-834-3
13	152.5	9.3	869	2	US-08-644-271-29
14	152	9.3	95	4	US-08-328-383B-18
15	150.5	9.2	698	2	US-08-601-725-36
16	150.5	9.2	734	2	US-08-389-459A-17
17	150.5	9.2	734	3	US-08-387-857A-17
18	147	9.0	365	4	US-08-928-383B-23
19	147	9.0	365	4	US-08-328-383B-24
20	146.5	8.9	315	2	US-08-414-657D-47
21	146.5	8.9	338	2	US-08-414-657D-42
22	146.5	8.9	338	2	US-08-114-657D-43
23	145.5	8.9	252	2	US-08-414-657D-57
24	145.5	8.9	287	2	US-08-414-657D-49
25	145.5	8.9	310	2	US-08-114-657D-45
26	145.5	8.9	338	2	US-08-114-657D-60
27	145.5	8.9	478	5	US-09-524-531a-15

PS Claim 1; Fig 3; 59pp; English.

PT

XX The present sequence is the human confluence regulated adhesion molecule

CC 1 (CRAM-1, also known as JAM-2). CRAM-1 is one of the vascular adhesion

CC proteins of the immunoglobulin superfamily (Ig SF). The CRAM-1 protein

CC and coding sequence can be used in the treatment of cancer, inflammation,

CC inflammation, to modulate cell-cell interactions and angiogenesis, and

CC in the modulation of wound healing.

XX Sequence 310 AA;

Query Match 100 %; Score 1633; DB 21; Length 310;

Best Local Similarity 100.0%; Pred. No. 3.6e-124; Matches 310; Conservati

0; Gaps 0; Mismatches 0; Indels 0;

QY 1 MALSRRLRLRYARAPHEFFILLFRQCMTEAVNLKSSNRNPVHREFESVLCITHSQT 60

Db 1 malstrrlrlryaraphffillfrqcmteavnlkssnrnpvhefesvlscithsqt 60

QY 61 SDPRLEWKKIQLDGQTYVYVYDNDKICDLAGRTDVGKTSLRINWNTRSDAIYRC

Db 61 sdprlewkkiqldgqqttyvydndkicdlagrtdvgktslrinwntrsdaiyrc 120

QY 121 NDRKEVDETEELIYKVPTPVCHIAPAVPGKATLQOCESQYPRPHYSWNRDVL 180

Db 121 ndrkevdeieliykvptpvchiapavpgkatiqocesqyprphyswrdv 180

QY 181 PTDSRANPQQNSHVNVSETGLYFNAVKDDSQYCITASNDAGARCEGQDMEVYL 240

Db 181 ptdsranprqnsfhnvsetgtlvfnavkddsqyycitasndagaarcegqdmeyd 240

QY 241 NIAGITGGVVLVLIHAVITNGICCAVRRGCFISSKQDGESYKSGKHDGNYRTSEEG 300

Db 241 niagiggivvliavitingiccaavrrgcfisskqdgesykspgkhgynyrtseeg 300

QY 301 DFRHSSFVI 310

Db 301 dfrhssfvi 310

RESULT 2
ID AAB27278
ID AAB27278 standard; Protein; 310 AA.XX
AC AAB27278;
XX DT 13-FEB-2001 (first entry)

XX DE Kurine confluence regulated adhesion molecule 1.

XX KW immunoglobulin superfamily; Ig SF; vascular adhesion molecule;

KW inflammation; cancer; wound; angiogenesis; mouse;

KW confluence regulated adhesion molecule 1; CRAM-1; JAM-2.

OS MUS SP.

XX PN WO200053749-A2.

XX PD 14-SEP-2000.

XX PF 13-MAR-2000; 2000WO-EP02219.

XX PR 11-MAR-1999; 99EP-0200746.

XX PA (RMFD-) RMF DICTAGENE SA.

XX PD Imhof BA, Aurrand-Lions M;

XX DR WPI; 2000-587436/55.

PT CRAM-2) polypeptide, useful for treatment of tumors, inflammation

XX reactions and modulating vascular permeability

XX Example; Fig 8; 59pp; English.

XX The present sequence is the murine confluence regulated adhesion molecule

CC 1 (CRAM-1, also known as JAM-2). CRAM-1 is one of the vascular adhesion

CC proteins of the immunoglobulin superfamily (Ig SF). The CRAM-1 protein

CC and coding sequence can be used in the treatment of cancer, inflammation,

CC to modulate cell-cell interactions and angiogenesis, and in the

CC modulation of wound healing.

XX Sequence 310 AA;

Query Match 100 %; Score 1633; DB 21; Length 310;

Best Local Similarity 100.0%; Pred. No. 3.6e-124; Matches 310; Conservati

0; Gaps 0; Mismatches 0; Indels 0;

QY 1 MALSRRLRLRYARAPHEFFILLFRQCMTEAVNLKSSNRNPVHREFESVLCITHSQT 60

Db 1 malstrrlrlryaraphffillfrqcmteavnlkssnrnpvhefesvlscithsqt 60

QY 61 SDPRLEWKKIQLDGQTYVYVYDNDKICDLAGRTDVGKTSLRINWNTRSDAIYRC

Db 61 sdprlewkkiqldgqqttyvydndkicdlagrtdvgktslrinwntrsdaiyrc 120

QY 121 NDRKEVDETEELIYKVPTPVCHIAPAVPGKATLQOCESQYPRPHYSWNRDVL 180

Db 121 ndrkevdeieliykvptpvchiapavpgkatiqocesqyprphyswrdv 180

QY 181 PTDSRANPQQNSHVNVSETGLYFNAVKDDSQYCITASNDAGARCEGQDMEVYL 240

Db 181 ptdsranprqnsfhnvsetgtlvfnavkddsqyycitasndagaarcegqdmeyd 240

QY 241 NIAGITGGVVLVLIHAVITNGICCAVRRGCFISSKQDGESYKSGKHDGNYRTSEEG 300

Db 241 niagiggivvliavitingiccaavrrgcfisskqdgesykspgkhgynyrtseeg 300

QY 301 DFRHSSFVI 310

Db 301 dfrhssfvi 310

RESULT 3
ID AAB27276
ID AAB27276 standard; Protein; 310 AA.XX
AC AAB27276;
XX DT 23-FEB-2001 (first entry)

XX DE Human confluence regulated adhesion molecule 1 #2.

XX KW immunoglobulin superfamily; Ig SF; vascular adhesion molecule;

KW inflammation; cancer; wound; angiogenesis; human;

KW confluence regulated adhesion molecule 1; CRAM-1; JAM-2.

OS Homo sapiens.

XX PN WO200053749-A2.

XX PR 14-SEP-2000.

XX PF 13-MAR-2000; 2000WO-EP02219.

XX PR 11-MAR-1999; 99EP-0200746.

XX PA (RMFD-) RMF DICTAGENE SA.

XX PR Imhof BA, Aurrand-Lions M;

XX DR WPI; 2000-587436/55.

DR N-PSDB: AAA95306.
 XX
 PT Isolated human Confluency Regulated Adhesion Molecule 1 or 2 (CRAM-1 or
 PT CRAM-2) polypeptide, useful for treatment of tumors, inflammation
 PT reactions and modulating vascular permeability -
 XX
 PS Claim 2; Fig 6; 59pp; English.

The present sequence is the human confluency regulated adhesion molecule 1 (CRAM-1, also known as JAM-2). CRAM-1 is one of the vascular adhesion proteins of the immunoglobulin superfamily (Ig Sf). The CRAM-1 protein and coding sequence can be used in the treatment of cancer, inflammation, to modulate cell-cell interactions and angiogenesis, and in the modulation of wound healing.

XX Sequence 310 AA:
 SQ

Y	Match	Score	Length	DB	21:	Length	310;	
Best Local Similarity	86.3%	Score	1409;	DB	21:	Length	310;	
Lines	85.8%;	Pred.	No.	4	5e-105;	Gaps	0;	
266;	Conservative			18;	Mismatches	0;		
Qy	1	MALSRRLRLYARLPHFFLLRFGCMIEAVNLKSSNRNPVWHEFSEVLSCTHSQT	60	Db	1 malrpprprlcarlpdpffllfrgcligavnlksnrtpvqrefesveiscltdsq	60	PR	08-MAR-1999; 99WO-US05028.
Qy	61	SDPRRIENKKIQDGOTTVWYFDNKKIQGDLAGRTDVFKGKUSLTWNWTRSDATYRCEVAL	120	Db	61 sdpriewkkkiqeqttvffdkqkqgddalaigtsklkwntvrdsalrycevar	120	PR	10-MAR-1999; 99US-0123618.
Qy	121	NDRKEVDEITLIVLIVOKPVPMVCRITAAPVKGATLQOCBSEGPYPRPHYSWYRDVPL	180	Db	121 narkeldeivleltvqkvptvpcrvkavpgmatahcgeseqhprrhyswyrndvpl	180	PR	12-MAR-1999; 99US-0123957.
Qy	181	PDSRANPFRQNSFRNSETGTLFVNAVKHDGQYCLIASNDAGARCEQDMEVYL	240	Db	181 pdtsranprfrnssfhlnsetgtlvftavkhdkdsgqyriasndagsarceeqemeydl	240	PR	23-MAR-1999; 99US-0125755.
Qy	241	NTAGIGGVLVVLLAVAVITMGICCAVRRGCFTISKODGESYKSPGKHDGVVWITSEEG	300	Db	241 niggigggvllvllavialitigicayrrgyfinkqdgesyknpgkpdgnyirtdeeg	300	PR	24-MAR-1999; 99US-0132371.
Qy	301	DPRHKSSFVI 310		Db	301 dfrhkssfvi 310		PR	04-MAY-1999; 99US-0134287.
Db	301	dfrhkssfvi 310					PR	02-JUN-1999; 99WO-0131252.
RESULT	4						PR	23-JUN-1999; 99WO-0141037.
AI	57						PR	20-JUL-1999; 99US-0144758.
IM	AB33457	standard; Protein; 310 AA.					PR	26-JUL-1999; 99US-014598.
AC	AAB33457;						PR	28-JUL-1999; 99US-0146222.
XX							PR	01-SEP-1999; 99WO-US20111.
DT	29-JAN-2001 (first entry)						PR	08-SEP-1999; 99WO-US20594.
XX							PR	13-SEP-1999; 99WO-US20944.
DE	Human PRO1668 protein UNQ859 SEQ ID NO:193.						PR	15-SEP-1999; 99WO-US21090.
XX							PR	15-SEP-1999; 99WO-US21547.
KW	Human; immune related disease; diagnosis; antiinflammatory; cardiot;						PR	03-OCT-1999; 99WO-US23089.
KW	dermatological; antiarthritic; antirheumatic; immunosuppressive;						PR	08-SEP-1999; 99WO-US20594.
KW	haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;						PR	13-SEP-1999; 99WO-US20944.
KW	antihaemac; hepatotoxic; virucide; antipsoriac; antiallergic;						PR	15-SEP-1999; 99WO-US21090.
KW	antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;						PR	15-SEP-1999; 99WO-US21547.
KW	osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;						PR	03-OCT-1999; 99WO-US23089.
KW	idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;						PR	08-SEP-1999; 99WO-US20594.
KW	systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;						PR	13-SEP-1999; 99WO-US20944.
KW	autoimmune thrombocytopenia; immune-mediated renal disease;						PR	15-SEP-1999; 99WO-US21090.
KW	demyelinating disease; hepatobiliary disease; Whipple's disease;						PR	15-SEP-1999; 99WO-US21547.
KW	inflammatory bowel disease; gluten-sensitive enteropathy;						PR	03-OCT-1999; 99WO-US23089.
KW	autoimmune disease; immune-mediated skin disease; allergic disease;						PR	08-SEP-1999; 99WO-US20594.
KW	immunological disease; transplantation associated disease;						PR	13-SEP-1999; 99WO-US20944.
KW	graft rejection; graft-versus-host disease.						PR	15-SEP-1999; 99WO-US21090.
XX	homo sapiens.						PR	15-SEP-1999; 99WO-US21547.
OS							PR	15-SEP-1999; 99WO-US21090.
XX							PR	15-SEP-1999; 99WO-US21547.
XX							PR	15-SEP-1999; 99WO-US21090.
XX							PR	15-SEP-1999; 99WO-US21547.
XX							PR	15-SEP-1999; 99WO-US21090.
XX							PR	15-SEP-1999; 99WO-US21547.
XX							PR	15-SEP-1999; 99WO-US21090.
XX							PR	15-SEP-1999; 99WO-US21547.
XX							PR	15-SEP-1999; 99WO-US21090.
XX							PR	15-SEP-1999; 99WO-US21547.
XX							PR	15-SEP-1999; 99WO-US21090.
XX							PR	15-SEP-1999; 99WO-US21547.
XX							PR	15-SEP-1999; 99WO-US21090.
XX							PR	15-SEP-1999; 99WO-US21547.
XX							PR	15-SEP-1999; 99WO-US21090.
XX							PR	15-SEP-1999; 99WO-US21547.
XX							PR	15-SEP-1999; 99WO-US21090.
XX							PR	15-SEP-1999; 99WO-US21547.
XX							PR	15-SEP-1999; 99WO-US21090.
XX							PR	15-SEP-1999; 99WO-US21547.
XX							PR	15-SEP-1999; 99WO-US21090.
XX							PR	15-SEP-1999; 99WO-US21547.
XX							PR	15-SEP-1999; 99WO-US21090.
XX							PR	15-SEP-1999; 99WO-US21547.
XX							PR	15-SEP-1999; 99WO-US21090.
XX							PR	15-SEP-1999; 99WO-US21547.
XX							PR	15-SEP-1999; 99WO-US21090.
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XX							PR	15-SEP-1999; 99WO-US21090.
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XX							PR	15-SEP-1999; 99WO-US21090.
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XX							PR	15-SEP-1999; 99WO-US21547.
XX							PR	15-SEP-1999; 99WO-US21090.
XX							PR	15-SEP-1999; 99WO-US21547.
XX							PR	15-SEP-1999; 99WO-US21090.
XX							PR	15-SEP-1999; 99WO-US21547.
XX							PR	15-SEP-1999; 99WO-US21090.
XX							PR	15-SEP-1999; 99WO-US21547.
XX							PR	15-SEP-1999; 99WO-US21090.
XX							PR	15-SEP-1999; 99WO-US21547.
XX							PR	15-SEP-1999; 99WO-US21090.
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XX							PR	15-SEP-1999; 99WO-US21090.
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XX							PR	15-SEP-1999; 99WO-US21090.
XX							PR	15-SEP-1999; 99WO-US21547.
XX							PR	15-SEP-1999; 99WO-US21090.
XX							PR	15-SEP-1999; 99WO-US21547.
XX							PR	15-SEP-1999; 99WO-US21090.
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XX							PR	15-SEP-1999; 99WO-US21090.
XX							PR	15-SEP-1999; 99WO-US21547.
XX							PR	15-SEP-1999; 99WO-US21090.
XX							PR	15-SEP-1999; 99WO-US21547.
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XX							PR	15-SEP-1999; 99WO-US21090.
XX							PR	15-SEP-1999; 99WO-US21547.
XX							PR	15-SEP-1999; 99WO-US21090.
XX							PR	15-SEP-1999; 99WO-US21547.
XX							PR	15-SEP-1999; 99WO-US21090.
XX							PR	15-SEP-1999; 99WO-US21547.
XX							PR	15-SEP-1999; 99WO-US21090.
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XX							PR	15-SEP-1999; 99WO-US21090.
XX							PR	15-SEP-1999; 99WO-US21547.
XX							PR	15-SEP-1999; 99WO-US21090.
XX							PR	15-SEP-1999; 99WO-US21547.
XX							PR	15-SEP-1999; 99WO-US21090.
XX							PR	15-SEP-1999; 99WO-US21547.
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XX							PR	15-SEP-1999; 99WO-US21547.
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XX							PR	15-SEP-1999; 99WO-US21547.
XX							PR	15-SEP-1999; 99WO-US21090.
XX							PR	15-SEP-1999; 99WO-US21547.
XX							PR	15-SEP-1999; 99WO-US210

Db	121	ndrkeideivieltvqkpvtpcrvpkavpgkmatlhcqeseghprphswryndvpl	180	CC	The present sequence is one of sixty one novel secreted and transmembrane PRO polypeptides. The PRO polypeptides are useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma), gastrointestinal disorders (e.g. enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's disease), wound repair, cardiovascular disorders (e.g. endometrial bleeding angiogenesis, ischaemias such as coronary ischaemia, atherosclerosis), inflammatory disorders (e.g. asthma, rheumatoid arthritis, multiple sclerosis), infertility, AIDS and diabetes and retinal disorders such as retinitis pigmentosum. The PRO nucleic acids have applications in molecular biology, including use as hybridization probes, and in chromosome and gene mapping.
Qy	181	PTDSRANRPFQNSFHVNSETGTLVFNVAHKDQSGQYCIAASNDAGARCEQDMEVYDL	240	CC	
Db	181	ptdsranprfrnssfhnsetgtlvftavkdsgqyyciasndagsarceeqemeydl	240	CC	
Qy	241	NTAGIIGGVLYLVLAVITMGICCAVRRGCFTSSKDGESTKSPGHDGVWYIRTSBEG	300	CC	
Db	241	niggigggvvlavallitigicayrrgyfinkqdgesyknpgkpdgvnyirtdeeg	300	CC	
Qy	301	DFRKSSVVI 310		CC	
Db	301	dfrkssvvi 310		CC	
RESULT	6			XX	Sequence 310 AA:
ID	AAB80272	standard; Protein: 310 AA.		XX	
AC	AAB80272;			XX	
DT	24-APR-2001 (first entry)			XX	
DE	Human PRO1868 protein.			XX	
XX	Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory; antiparkinsonian; nototropic; neuroprotective; vulnerary; cardiant; antiangiogenic; vasoactive; antiasthmatic; antirheumatic; cancer; antiinflammatory; antidiabetic; antiviral; diabetes; ophthalmological; gene therapy; skin disease; gastrointestinal disorder; ischaemia; inflammation.			XX	
KW				XX	
OS	Homo sapiens.			XX	
PN	WO200104311-A1.			XX	
PD	18-JAN-2001.			XX	
XX				XX	
PF	22-FEB-2000; 2000WO-US04414.			XX	
PR	07-JUL-1999; 99US-0143048.			XX	
PR	26-JUL-1999; 99US-0145698.			XX	
PR	15-SEP-1999; 99US-0521547.			XX	
PR	05-OCT-1999; 99US-0523089.			XX	
PR	22-NOV-1999; 99WO-US28214.			XX	
PR	03-NOV-1999; 99WO-US28313.			XX	
PR	16-DEC-1999; 99WO-US30095.			XX	
PR	20-DEC-1999; 99WO-US30911.			XX	
PR	20-DEC-1999; 99WO-US30999.			XX	
PR	05-JAN-2000; 99WO-US500219.			XX	
PA	(GPTH) GENENTECH INC.			XX	
XX				XX	
PT	Ashkenazi AJ, Botstein D, Desnoyers L, Eaton DL, Ferrara N; Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Godowski PJ, Grimaldi CJ, Gurney AL, Hillian KJ, Kijavin JU; Mather JP, Pan J, Paoletti NF, Roy MA, Stewart TA, Tumas D; Williams PM, Wood WI;			XX	
PI	XX			XX	
DR	WPI: 2001-081051/09.			XX	
DR	N-PSDB; AAF7243.			XX	
XX	Sixty one nucleic acids encoding PRO polypeptides which are useful in the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma) and neurodegenerative diseases (e.g. Alzheimer's disease).			XX	
PS	Claim 1; Fig 124; 393pp; English.			XX	
RESULT	7			XX	Query Match 86.3%; Score 1409; DB 22; Length 310; Best Local Similarity 85.8%; Pred. NO. 4.5e-106; Matches 266; Conservative 18; Mismatches 26; Indels 0; Gaps 0;
ID	AAB80383	standard; protein: 310 AA.		XX	
AC	AAB80383;			XX	
DT	24-APR-2001 (first entry)			XX	
DE	Secreted protein encoded by gene #13.			XX	
KW	Secreted protein; human; autoimmune; hyperproliferation; cardiovascular; cerebrovascular; infection; food.			XX	
KW				XX	
OS	Homo sapiens.			XX	
PN	WO200107459-A1.			XX	
PD	01-FEB-2001.			XX	
PF	20-JUL-2000; 2000WO-US19735.			XX	
PR	23-JUL-1999; 99US-0145220.			XX	
PA	(HUMA-) HUMAN GENOME SCI INC.			XX	
PI	Rosen CA, Ruben SM, Ebner R, Duan RD, Ni J, Soppet DR, Moore PA; Shi Y, Lafleur DM, Olsen HS, Birse CE, Komatsu S; GA;			XX	

CC disorders e.g. corneal infection. The polypeptides can also be used to
 CC aid wound healing and epithelial cell proliferation, to prevent skin
 CC aging due to sunburn, to maintain organs before transplantation, for
 CC supporting cell culture of primary tissues, to regenerate tissues and in
 CC chemotaxis.

XX Sequence 311 AA;

Query Match Similarity 86.3%; Score 1409; DB 21; Length 311;
 Best Local Similarity 85.8%; Pred. No. 4.5e-106; Mismatches 26; Indels 0; Gaps 0;
 Matches 266; Conservative 18; Mismatches 26; Indels 0; Gaps 0;

PS Disclosure: Page 75; 601pp; English.
 XX
 CC The present invention relates to 29 human secreted proteins. The
 CC invention is used to prevent autoimmune diseases e.g. rheumatoid
 CC arthritis, hyperproliferative disorders e.g. neoplasms of the
 CC breast or liver, cardiovascular disorders e.g. cerebral ischemia, angiogenesis,
 CC cerebrovascular disorders e.g. Alzheimer's disease, infections
 CC nervous system disorders e.g. Alzheimer's disease, infections
 CC caused by bacteria, viruses and fungi and ocular disorders e.g.
 CC corneal infection. Also used in food preparations.

XX Sequence 339 AA;

Query Match Similarity 86.3%; Score 1409; DB 22; Length 339;
 Best Local Similarity 85.8%; Pred. No. 5e-106; Mismatches 26; Indels 0; Gaps 0;
 Matches 266; Conservative 18; Mismatches 26; Indels 0; Gaps 0;

PS Disclosure: Page 75; 601pp; English.
 XX
 CC The present invention relates to 29 human secreted proteins. The
 CC invention is used to prevent autoimmune diseases e.g. rheumatoid
 CC arthritis, hyperproliferative disorders e.g. neoplasms of the
 CC breast or liver, cardiovascular disorders e.g. cerebral ischemia, angiogenesis,
 CC cerebrovascular disorders e.g. Alzheimer's disease, infections
 CC nervous system disorders e.g. Alzheimer's disease, infections
 CC caused by bacteria, viruses and fungi and ocular disorders e.g.
 CC corneal infection. Also used in food preparations.

QY 1 MAISRLRLYALRPHFELLFRGCMTEAVNKKSSNRPVHEFESVELSCITHSQT 60
 ||||| ||||| ||||| ||||| : ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1 malkrpprirlcarlpdflllfrgcilgavnlksnrtpvqgeffesvelscitdsqt 60
 QY 61 SDPPIEWKKIQDGOTTYFDFNKIQDLAGRTDVGKTSRLIRNWNTSDA1RCEVAL 120
 ||||| ||||| ||||| ||||| : ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 61 sdpielkkidqedttvqkpvtpvprvkvpgvpgmatahcgeseqhprrhswrndpl 180
 C 121 NDREVEDETTIELVQVKPVTPVCRIPAAVPVGSTATQCQESGYPRPHYSWRNDPL 180
 ||||| ||||| ||||| ||||| : ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 121 ndrkeideiweieltvqkpvtpvprvkvpgvpgmatahcgeseqhprrhswrndpl 180
 QY 181 PTDSRANPRFQNSFHVNETGTVLAVNFKHDSSGQYVCIASNDGARCEGDMEVYL 240
 ||||| ||||| ||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 181 ptdsranprfrnsfhinsetgtlvftavhkdssgqyqciashdasarcdeqemeyvd 240
 QY 241 NIAGIGGVLWVLVLAUTMGICCAVRRGCFISSKQDGEYSVSPKGHDGVNIRTSBEG 300
 ||||| ||||| ||||| : ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 241 niggliiggyvlwvlavlaflitlgicccayrrgffinnkqagesyknpgkpdgvnyirtdeeg 300
 QY 301 DFRKSSFV1 310
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 301 dfrikssfv1 310
 QY 301 DFRKSSFV1 310
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 330 dfrikssfv1 339

RESULT 13

ABB0431:
 XX
 ID AAB0431 standard; peptide; 339 AA.
 XX
 AC AAB0431:
 XX
 DT 24-APR-2001 (first entry)
 XX
 D Gene #13 associated peptide #11.
 XX
 K Secreted protein; human; autoimmune; hyperproliferation;
 XX
 K cardiovascular; cerebrovascular; infection; food.
 XX
 O Homo sapiens.
 XX
 PN WO200107459-A1.
 XX
 PD 01-FEB-2001.
 XX
 PF 20-JUL-2000; 2000000-US19735.
 XX
 PR 23-JUL-1999; 99US5-0145220.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Ruben SM, Ebner R, Duan RD, Ni J, Soppet DR, Moore PA;
 PI Shi Y, Lafleur DW, Olsen HS, Birse CE, Komatsu S GA;
 XX
 WPI; 2001-123261/13.

XX
 PT New isolated nucleic acid encoding 29 secreted proteins, for
 PT diagnosing, preventing and treating e.g. autoimmune,
 PT hyperproliferative, cardiovascular, and ocular diseases or disorders
 PT and microorganism infections

PS Disclosure: Page 75; 601pp; English.
 XX
 CC The present invention relates to 29 human secreted proteins. The
 CC invention is used to prevent autoimmune diseases e.g. rheumatoid
 CC arthritis, hyperproliferative disorders e.g. neoplasms of the
 CC breast or liver, cardiovascular disorders e.g. cerebral ischemia, angiogenesis,
 CC cerebrovascular disorders e.g. Alzheimer's disease, infections
 CC nervous system disorders e.g. Alzheimer's disease, infections
 CC caused by bacteria, viruses and fungi and ocular disorders e.g.
 CC corneal infection. Also used in food preparations.

PS Disclosure: Page 75; 601pp; English.
 XX
 CC The present invention relates to 29 human secreted proteins. The
 CC invention is used to prevent autoimmune diseases e.g. rheumatoid
 CC arthritis, hyperproliferative disorders e.g. neoplasms of the
 CC breast or liver, cardiovascular disorders e.g. cerebral ischemia, angiogenesis,
 CC cerebrovascular disorders e.g. Alzheimer's disease, infections
 CC nervous system disorders e.g. Alzheimer's disease, infections
 CC caused by bacteria, viruses and fungi and ocular disorders e.g.
 CC corneal infection. Also used in food preparations.

QY 1 MAISRLRLYALRPHFELLFRGCMTEAVNKKSSNRPVHEFESVELSCITHSQT 60
 ||||| ||||| ||||| ||||| : ||||| ||||| ||||| ||||| ||||| |||||
 Db 1 malkrpprirlcarlpdflllfrgcilgavnlksnrtpvqgeffesvelscitdsqt 60
 QY 61 SDPPIEWKKIQDGOTTYFDFNKIQDLAGRTDVGKTSRLIRNWNTSDA1RCEVAL 120
 ||||| ||||| ||||| : ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 61 sdpielkkidqedttvqkpvtpvprvkvpgvpgmatahcgeseqhprrhswrndpl 180
 C 121 NDREVEDETTIELVQVKPVTPVCRIPAAVPVGSTATQCQESGYPRPHYSWRNDPL 180
 ||||| ||||| ||||| : ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 121 ndrkeideiweieltvqkpvtpvprvkvpgvpgmatahcgeseqhprrhswrndpl 180
 QY 181 PTDSRANPRFQNSFHVNETGTVLAVNFKHDSSGQYVCIASNDGARCEGDMEVYL 240
 ||||| ||||| ||||| : ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 181 ptdsranprfrnsfhinsetgtlvftavhkdssgqyqciashdasarcdeqemeyvd 240
 QY 241 NIAGIGGVLWVLVLAUTMGICCAVRRGCFISSKQDGEYSVSPKGHDGVNIRTSBEG 300
 ||||| ||||| ||||| : ||||| ||||| ||||| ||||| ||||| |||||
 Db 241 niggliiggyvlwvlavlaflitlgicccayrrgffinnkqagesyknpgkpdgvnyirtdeeg 300
 QY 301 DFRKSSFV1 310
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 330 dfrikssfv1 339

PS Disclosure: Page 75; 601pp; English.
 XX
 CC The present invention relates to 29 human secreted proteins. The
 CC invention is used to prevent autoimmune diseases e.g. rheumatoid
 CC arthritis, hyperproliferative disorders e.g. neoplasms of the
 CC breast or liver, cardiovascular disorders e.g. cerebral ischemia, angiogenesis,
 CC cerebrovascular disorders e.g. Alzheimer's disease, infections
 CC nervous system disorders e.g. Alzheimer's disease, infections
 CC caused by bacteria, viruses and fungi and ocular disorders e.g.
 CC corneal infection. Also used in food preparations.

PS Disclosure: Page 75; 601pp; English.
 XX
 CC The present invention relates to 29 human secreted proteins. The
 CC invention is used to prevent autoimmune diseases e.g. rheumatoid
 CC arthritis, hyperproliferative disorders e.g. neoplasms of the
 CC breast or liver, cardiovascular disorders e.g. cerebral ischemia, angiogenesis,
 CC cerebrovascular disorders e.g. Alzheimer's disease, infections
 CC nervous system disorders e.g. Alzheimer's disease, infections
 CC caused by bacteria, viruses and fungi and ocular disorders e.g.
 CC corneal infection. Also used in food preparations.

AC AAB39254;
 XX
 PF 02-FEB-2001 (first entry)
 XX
 PR Human secreted protein sequence encoded by gene 15 SEQ ID NO:134.
 PR DE
 PR XX
 PR Human; secreted protein; immunosuppressive; antiarthritic; antirheumatic;
 PR antiproliferative; cytostatic; cardiotropic; vasotropism; cerebroprotective;
 PR nootropic; neuroprotective; antibacterial; virucide; fungicide; neoplasm;
 PR ophthalmological; autoimmune disease; rheumatoid arthritis; angiogenesis;
 PR hyperproliferative disorder; cardiovascular disorder; infection;
 PR cerebrovascular disorder; nervous system disorder; ocular disorder;
 PR KW wound healing; chemotaxis.
 XX
 PT Homo sapiens.
 XX
 PT WO200056754-A1.
 XX
 PN 28-SEP-2000.
 XX
 PT 16-MAR-2000; 2000WO-US06792.
 XX
 PR 19-MAR-1999; 99US-0125562.
 PR 10-DEC-1999; 99US-0169880.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PT Rosen GA, Ruben SM, Komatsoulis G;
 XX
 DR WPI; 2000-579483/54.
 DR N-PSDB; AAC74237.
 XX
 PT Isolated nucleic acid molecule encoding a human secreted protein is
 PT used in preventing, treating or ameliorating a medical condition.
 XX
 PS Disclosure; Page 32; 434pp; English.
 XX
 CC The polynucleotide sequences given in AAC7423-C74279 encode the human
 CC secreted proteins represented in AAB39179-B39226. Sequences
 CC AAB3927-B39308 are alternative proteins encoded by the genes, and also
 CC protein sequences with which they share homology. The proteins have
 CC activities based on the tissues and cells in which they are expressed.
 CC Examples of activities include: immunosuppressive; antiarthritic;
 CC anti-rheumatic; antiproliferative; cytostatic; cardiotropic; vasotropism;
 CC cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
 CC fungicidal; and ophthalmological. The human secreted proteins,
 CC polynucleotides and antagonists and agonists of the invention may be useful
 CC in the treatment, prevention, and/or diagnosis of various disease,
 CC disorders and conditions such as autoimmune diseases e.g. rheumatoid
 CC arthritis, hyperproliferative disorders e.g. neoplasms of the breast or
 CC liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular
 CC disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders
 CC e.g. Alzheimer's disease, infections caused by bacteria, viruses, fungi and ocular disorders e.g. corneal infection. The polypeptides can
 CC also be used to aid wound healing and epithelial cell proliferation, to
 CC regenerate tissues, maintain organs before transplantation, to
 CC chemotaxis and as a food additive or preservative e.g. to increase
 CC storage capabilities. Sequences AAC74214-C74222 and AAB3918 are used
 CC during the isolation and characterisation of the genes of the invention.
 XX
 SQ Sequence 310 AA;
 Query Match 85.8%; Score 1401; DB 21; Length 310;
 Best Local Similarity 85.5%; Pred. No. 2e-105;
 Matches 265; Conservative 18; Mismatches 27; Indels 0; Gaps 0;
 PT
 Qy 1 MALSRKURLYARPPHFFULLPRGCMIEAVNLKSSNRNPVWHEFSEVELSCITHSQ 60
 Db 1 malrrprpricaripdfllffrgclgavnnkssnrnpvqffesvelscitldsq 60
 Qy 61 SDPREFWKKQDGQTYVYFVKNDLAGRDVFGKTSRIRWNTRSDAIYREVAL 120
 Db 61 sdprkewkkqdeqtfyffankqldqraelgktskwntrrdsalyrevar 120
 Qy 121 NDRKEVDEITELIVQVKPVPVCRIPAAVPGKATLOCOESQEPYPPRIVSWYNDVPL 180
 Db 121 nrdkeledeiveltqvkpvvpvcrtpkavpgknhthqesehprphyswryndvpl 180
 Qy 181 PTDSPRANPRQNSSEPVNNESTGILVNAVKDDSOYCYCASNDGARCEGQDMEVYL 240
 Db 181 ptdspranprnsshlnsetgtlyftavkhkdsgqycciasndgssarceeqeveyd 240
 Qy 241 NIAGIGGVLVVLIVLAVIYRGGFISKQDGESYKSKGHDENVYRUSEEG 300
 Db 241 niggiggvvlvlalitigicayrgrgyfinkqdgesykgpkpdvnyirtdeeg 300
 Qy 301 DFRHKSFSV 310
 Db 301 dfrhksfsv 310
 RESULT 15
 ABA2254 standard; protein; 285 AA.
 XX AAB39254;
 XX
 PR 02-FEB-2001 (first entry)
 XX
 PR Human secreted protein sequence encoded by gene 15 SEQ ID NO:134.
 PR DE
 PR XX
 PR Human; secreted protein; immunosuppressive; antiarthritic; antirheumatic;
 PR antiproliferative; cytostatic; cardiotropic; cerebroprotective;
 PR nootropic; neuroprotective; antibacterial; virucide; fungicide; neoplasm;
 PR ophthalmological; autoimmune disease; rheumatoid arthritis; angiogenesis;
 PR hyperproliferative disorder; cardiovascular disorder; infection;
 PR cerebrovascular disorder; nervous system disorder; ocular disorder;
 PR KW wound healing; chemotaxis.
 XX
 PT Homo sapiens.
 XX
 PT WO200056754-A1.
 XX
 PN 28-SEP-2000.
 XX
 PT 16-MAR-2000; 2000WO-US06792.
 XX
 PR 19-MAR-1999; 99US-0125562.
 PR 10-DEC-1999; 99US-0169880.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PT Rosen GA, Ruben SM, Komatsoulis G;
 XX
 DR WPI; 2000-579483/54.
 DR N-PSDB; AAC74237.
 XX
 PT Isolated nucleic acid molecule encoding a human secreted protein is
 PT used in preventing, treating or ameliorating a medical condition.
 XX
 PS Disclosure; Page 32; 434pp; English.
 XX
 CC The polynucleotide sequences given in AAC7423-C74279 encode the human
 CC secreted proteins represented in AAB39179-B39226. Sequences
 CC AAB3927-B39308 are alternative proteins encoded by the genes, and also
 CC protein sequences with which they share homology. The proteins have
 CC activities based on the tissues and cells in which they are expressed.
 CC Examples of activities include: immunosuppressive; antiarthritic;
 CC anti-rheumatic; antiproliferative; cytostatic; cardiotropic; vasotropism;
 CC cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
 CC fungicidal; and ophthalmological. The human secreted proteins,
 CC polynucleotides and antagonists and agonists of the invention may be useful
 CC in the treatment, prevention, and/or diagnosis of various disease,
 CC disorders and conditions such as autoimmune diseases e.g. rheumatoid
 CC arthritis, hyperproliferative disorders e.g. neoplasms of the breast or
 CC liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular
 CC disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders
 CC e.g. Alzheimer's disease, infections caused by bacteria, viruses, fungi and ocular disorders e.g. corneal infection. The polypeptides can
 CC also be used to aid wound healing and epithelial cell proliferation, to
 CC regenerate tissues, maintain organs before transplantation, to
 CC chemotaxis and as a food additive or preservative e.g. to increase
 CC storage capabilities. Sequences AAC74214-C74222 and AAB3918 are used
 CC during the isolation and characterisation of the genes of the invention.
 XX
 SQ Sequence 285 AA;
 Query Match 80.4%; Score 1313; DB 21; Length 285;
 Best Local Similarity 85.6%; Pred. No. 2.3e-98;
 Matches 244; Conservative 18; Mismatches 23; Indels 0; Gaps 0;
 PT
 Qy 26 GCMIEAVNLKSSNRNPVWHEFSEVELSCITHSQSDPREFWKKQDGQTYVYFDNKIQ 85
 Db 1 qclgavnnkssnrnpvqffesvelscitldsqsdprkewkkqdeqtfyffankqldqraelgktskwntrrdsalyrevar 60
 Qy 86 DGLAGRIVFGKTSRIRWNTRSDAIYREVALNDREVEDEITELIVQVKVTPVCR 145

Db 61 gdlagraeilgtsklivnvrtrdsalyrcervarnarkideivieltvqkpvtpvcr 120
Qy 146 IPAVVPGKTATLQCQSEGYPPRHYSWNRNDVPLPTDSRANPRFQNSFHNSETGTLV 205
Db 121 vpkxvpgkmatihcqegehphprphyswvrdplptdsranprfrnsfhlinstgtlv 180
Qy 206 FNAVHKDGSQYCTASNDAGARCEGDMEVYDLNTAGITGGVLUVLLAVTMICC 265
Db 181 ftavhkdasqyyrciasndagsarceeqemeydlnigilqvlvlavialitlgicc 240
Qy 266 AVRRGCFLSSKQDGEVKSPKGKUDGVNIRTSEGDERRHKSFTI 310
Db 241 ayrrgyfinkqdggesyknpgkpdgvyrteegdfhkssfvi 285

Search completed: August 6, 2001, 09:33:05
JTime: 216 sec

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XX Cunningham S, Trinidad Arrate Barros M;
 PT XX endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
 XX Homo sapiens.
 DR XX OS
 DR XX N-PSDB; AAS00512.
 XX PT Key
 XX PT Misc-difference 42
 PT FT Location/qualifiers
 PT FT /Label= unknown
 XX FN /Label= unknown
 PN W09840483-A2.
 XX PD 17-SEP-1998.
 XX PF 12-MAR-1998; 98WO-US04858.
 XX PR 19-DEC-1997; 97US-0040710.
 PR 14-MAR-1997; 97US-0040710.
 PR 14-MAR-1997; 97US-0040710.
 PR 30-MAY-1997; 97US-0048100.
 PR 30-MAY-1997; 97US-0048189.
 PR 30-MAY-1997; 97US-0048357.
 PR 30-MAY-1997; 97US-0050934.
 PR 06-JUN-1997; 97US-0048970.
 PR 05-SEP-1997; 97US-0057765.
 XX PA (HOMA-) HUMAN GENOME SCI INC.
 XX Ferrie AM, Fischer CL, Gentz RU, Greene JM, Kyaw H;
 PT Li H, Li Y, Moore PA, Rosen CA, Ruben SM, Soppet DR;
 PT Wei YF, Young PE, Zeng Z;
 XX DR WPI: 1998-520811/44.
 DR N-PSDB; AAV34310.
 XX PT Isolated human poly:nucleotide(s) encoding secretory peptide(s) used to develop products for the diagnosis and treatment of e.g. inflammation, cancers, CNS disorders or immune system disorders.
 XX Claim 1; Page 168-169; 201pp; English.
 CC This sequence represents a secreted human protein encoded by the gene clone detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. AAV34277) for increasing the stability of the fused protein as compared to the human protein only.
 CC The invention relates to 28 novel human genes and their fragments (nucleic acid sequences: AAV34206-VA3325; amino acid sequences AAV75196-W72335) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 28 polynucleotides, based on which tissues they are most highly expressed in (see AAV34286 for described uses).
 CC (see AAV34286 for described uses).
 XX Sequence 298 AA;

SQ Sequence 298 AA;

Query Match 30.9%; Score 505; DB 22; Length 298;
 Best Local Similarity 37.3%; Pred No 4.3e-33; Matches 118; Conservative 61; Mismatches 111; Indels 26; Gaps 9;
 CC
 QY 3 LSRRRLRLYARLPHFFLLFRGCMI----EAVNLKSSNRNPVH--EFSVELSCII 55
 DB 1 marrsrrhrl-----lllrrlylvalgylghkaygfsapkdgqvavxyjeailack-k 51
 QY 56 THSOTSDPRIKKIQDGOTTYVFDNKIQGDLAGRTDVFGRKTSLRWNWTSATYRC 115
 DB 52 tppkktvxsrllekkk--grsvsfyyqqlqgdknraemi-dfnirkvntsdagkyrc 109
 QY 116 EVAVLNDR-KEVBDITIELIVQVKPVTCR1AAVPVGKATLQCOSESEGYPYPHYSWY 174
 DB 110 evapsqeqgnleedtvtklevivapavpscevpssalsgtvvelrcqkengnnapewytwf 169
 QY 175 RNDVPLPPTDSRANPFRONFSFHVNSEGTLVFNWAKHDKDSGQYCTIASNDAGARCEGOD 234
 DB 170 kgdkrlllenprlgsqstnsyntmtktgllqfntvskitgeyscearnsvyrrcpktr 229
 QY 235 MEVVDLNTAGIIGVWLVLVILAVITMGCCAVRRGCFLSSKPDGEGSKMSPGKHDGVYI 294
 DB 230 mqyvadlinsigiaavvvavvalvisvcqgvcyadrgkyf--ske---tsfqksnsska 282
 QY 295 RTSEEGDFRHKSSWV 310
 DB 283 tttusendfthtksfii 298
 XX Sequence 298 AA;

SQ Sequence 298 AA;

Query Match 30.5%; Score 498; DB 19; Length 298;
 Best Local Similarity 37.0%; Pred No 1.6e-32; Matches 111; Conservative 61; Mismatches 112; Indels 26; Gaps 9;
 CC
 QY 3 LSRRRLRLYARLPHFFLLFRGCMI----EAVNLKSSNRNPVH--EFSVELSCII 55
 DB 1 marrsrrhrl-----lllrrlylvalgylghkaygfsapkdgqvavxyjeailack-k 51
 QY 56 THSOTSDPRIKKIQDGOTTYVFDNKIQGDLAGRTDVFGRKTSLRWNWTSATYRC 115
 DB 52 tppkktvxsrllekkk--grsvsfyyqqlqgdknraemi-dfnirkvntsdagkyrc 109
 QY 116 EVAVLNDR-KEVBDITIELIVQVKPVTCR1AAVPVGKATLQCOSESEGYPYPHYSWY 174

SQ Sequence 298 AA;

Db	110	evsabseqgnleedvtlevlavaavpscavpsalsgtwvelrcdkgengpapewtf	169
Qy	175	RNDVPLPTDSRANPRQNSHVNSETGTLVFNVAHKDDSGOYCTASNDGAAARCBGQD	234
Db	170	kdgirilenprlgsqstnqsyntktqtlqfntvskldtgyscearnsvyrrcpgr	229
Qy	235	MEVDYDNTAIGGVLVVLIVAVLAVITMGCCARRGCFISQKDGESYKSPKHDGNYI	294
Db	230	mqvdinlsgiaavvvalivisvcgqlyqcyarqgyf-ske----tsfqksnsska	282
Qy	295	RTSEEGOFRRHKSFVI 310	
Db	283	ttmsendfhtksfli 298	
RESULT 19			
ID	AAB27273	AAB27273 standard; Protein; 298 AA.	
XX			
AC			
XX			
DT			
XX			
DE			
XX			
DE		Human confluency regulated adhesion molecule 2 #1.	
XX			
KW		Immunoglobulin superfamily; Ig Sf; vascular adhesion molecule;	
KW		inflammation; cancer; wound; angiogenesis; human;	
KW		confluency regulated adhesion molecule 2; CRAM-2; JAM-3.	
OS		Homo sapiens.	
XX			
PN		WO20053749-A2.	
XX			
PD		14-SEP-2000.	
XX			
PF		13-MAR-2000; 2000WO-EP02219.	
XX			
PR		11-MAR-1999; 99EP-0200746.	
XX			
PA		(RMFD-) RMF DICTAGENE SA.	
XX			
PI		Imhof BA, Aurrand-Lions M;	
XX			
DR		WPI; 2000-587436/55.	
XX			
PT		Isolated human Confluency Regulated Adhesion Molecule 1 or 2 (CRAM-1 or	
PT		CRAM-2) polypeptide, useful for treatment of tumors, inflammation	
PT		reactions and modulating vascular permeability	
XX		aim 1; Fig 3; 59pp; English.	
PS			
XX			
CC		The present sequence is the human confluency regulated adhesion molecule	
CC		2 (CRAM-2, also known as JAM-3). CRAM-2 is one of the vascular adhesion	
CC		proteins of the immunoglobulin superfamily (Ig Sf). The CRAM-2 protein	
CC		and coding sequence can be used in the treatment of cancer, inflammation,	
CC		to modulate cell-cell interactions and angiogenesis, and in the	
CC		modulation of wound healing.	
XX			
SO		Sequence 298 AA:	
RESULT 20			
ID	AAB27275	AAB27275 standard; Protein; 298 AA.	
XX			
AC			
XX			
DT			
XX			
DE		Murine confluency regulated adhesion molecule 2.	
XX			
KW		Immunoglobulin superfamily; Ig Sf; vascular adhesion molecule;	
KW		inflammation; cancer; wound; angiogenesis; mouse;	
KW		confluency regulated adhesion molecule 2; CRAM-2; JAM-3.	
XX			
OS		Mus sp.	
XX			
PN		WO20053749-A2.	
XX			
PD		14-SEP-2000.	
XX			
PF		13-MAR-2000; 2000WO-EP02219.	
XX			
PR		11-MAR-1999; 99EP-0200746.	
XX			
PA		(RMFD-) RMF DICTAGENE SA.	
XX			
PI		Imhof BA, Aurrand-Lions M;	
XX			
DR		WPI; 2000-587436/55.	
XX			
PT		Isolated human Confluency Regulated Adhesion Molecule 1 or 2 (CRAM-1 or	
PT		CRAM-2) polypeptide, useful for treatment of tumors, inflammation	
PT		reactions and modulating vascular permeability	
XX		aim 1; Fig 3; 59pp; English.	
PS			
XX			
CC		The present sequence is the murine confluency regulated adhesion molecule	
CC		2 (CRAM-2, also known as JAM-3). CRAM-2 is one of the vascular adhesion	
CC		proteins of the immunoglobulin superfamily (Ig Sf). The CRAM-2 protein	
CC		and coding sequence can be used in the treatment of cancer, inflammation,	
CC		to modulate cell-cell interactions and angiogenesis, and in the	
CC		modulation of wound healing.	
XX			
SO		Sequence 298 AA:	

Db 61 rlewkvgg-vslwygqgalqgfdraemi-dfnirknvttsdageyrcvsaaptq 118
 Qy 124 -KEVDEITIELIVOKPVKPVCRIPAAVPGKTAQLOQESEGYPRPHSWYRNQDPLPT 182
 Db 119 gqniledkvmlevavapavpacevptsmtgsvvvercakgepapayiwfdg---t 174
 Qy 183 DSRANPR--FQNSFFHVNSETGFLVNAVKHDQSGQYCIAASNDAGARCEODMEYD 239
 Db 175 s15ngkqgthnnsytnesqgqfnniskndsgycearnsngvhrccpkrmqdr 234
 Qy 240 LNTAGIGGGLVVLLVAVITMGICCAVRRGCFTISKQDGESYKSPGKHGDGVNIRTSE 299
 Db 235 lnsigiaavvvvraffvisvcgllcyaqrkgf--sktsfqkqsp----askvttng 287.
 Qy 300 GDFRKSSRFV 310
 Db 288 ndfrhtksfli 298

REF 21
 AA 60
 ID AAY08060 standard; Protein; 312 AA.
 XX
 AC AAY08060;
 XX 11-SEP-2000 (first entry)
 DT XX
 DE Human PRO245 protein.
 XX
 KW Inflammatory cell infiltration; immune response; T cell proliferation;
 KW anti-inflammatory; anti-autoimmune; anti-diabetic; spondyloarthropathy;
 KW T cell-mediated disease; spondyloarthropathy; scleroderma; renal disease;
 KW inflammatory myopathy; hemolytic anemia; thrombocytopenia; spondyloarthropathy;
 KW diabetes mellitus; inflammatory bowel disease; Guillain-Barré syndrome;
 KW sclerosing cholangitis; demyelinating polyneuropathy; Whipple's disease;
 KW skin disease; dermatitis; psoriasis; asthma; eosinophilic pneumonia; transplant;
 KW food hypersensitivity; urticaria; allergic rhinitis; tumor;
 KW idiopathic pulmonary fibrosis; graft rejection; PRO245; human.
 OS Homo sapiens.
 XX
 PN W09914241-A2.
 PD 25-MAR-1999.
 PP 17-SEP-1998; 98WO-US19437.
 XX
 PR 07-SEP-1997; 97US-005119.
 PR 18-SEP-1997; 97US-0059263.
 PR 28-OCT-1997; 97US-0033550.
 PR 12-NOV-1997; 97US-0065186.
 PR 21-NOV-1997; 97US-0060364.
 PR 24-NOV-1997; 97US-0066770.
 PR 04-JUN-1998; 98US-0088026.
 PA (GETH) GENENTECH INC.
 PI Fong S, Goddard A, Gurney AL, Tumas D, Wood WI;
 XX
 DR WPI; 1999-22699/19.
 DR N-PSDB; AAX37664.

PS Example 1; Fig 2; 177pp; English.

PT Composition - containing novel polypeptide PRO245, its agonist or antagonist -
 XX
 PT antagonist -
 XX
 PS RESULT 22
 XX AAY23324
 ID AAY23324 standard; Protein; 312 AA.
 XX
 AC AAY23324;
 XX
 DT 02-SEP-1999 (first entry)
 XX
 DE A33 related antigen PRO245.

This invention describes a novel composition containing (apart from a carrier or excipient), a novel PRO245 polypeptide (I), its agonist or antagonist, or their fragments, for modulating: (i) infiltration of inflammatory cells into tissue; (ii) an immune response; or (iii) T cell proliferation. The composition increases or decreases any of the effects

CC (i)-(iii). The products of the invention have anti-inflammatory, anti-autoimmune and anti-diabetic activity. (I), and its (antagonists and their fragments are used to treat immune-related diseases, particularly T cell-mediated diseases. The diseases treated include systemic lupus erythematosus, rheumatoid arthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis (scleroderma), idiopathic inflammatory myopathies (dermatomyositis, polymyositis), Sjögren's syndrome, systemic vasculitis, sarcoidosis, autoimmune hemolytic anemia (immune pancytopenia, paroxysmal nocturnal hemoglobinuria), autoimmune thrombocytopenia (idiopathic thrombocytopenic purpura, immune-mediated thrombocytopenia), thyroditis (Graves disease, Hashimoto's thyroiditis, juvenile lymphocytic thyroiditis, atrophic thyroiditis), diabetes mellitus, immune-mediated renal disease (glomerulonephritis, tubulointerstitial nephritis), multiple sclerosis, idiopathic demyelinating polyneuropathy, Guillain-Barré syndrome, chronic inflammatory demyelinating polyneuropathy, infectious hepatitis (hepatitis A, B, C, D, E and other non-hepatotropic viruses), autoimmune hepatitis, primary biliary cirrhosis, granulomatous hepatitis, and sclerosing cholangitis, inflammatory bowel disease (ulcerative colitis; Crohn's disease), gluten-sensitive enteropathy, and Whipple's disease. Autoimmune or immune-mediated skin diseases including bullous skin diseases, erythema multiforme, contact dermatitis, psoriasis, urticaria, eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, and transplantation associated diseases (graft rejection, and graft-versus-host-disease). (I), its (antagonists or fragment can also be used as an adjuvant in treatment of tumors. Antibodies against (I) can also be used for diagnosing such diseases. This sequence represents the human PRO245 protein described in the invention.

CC Sequence 312 AA;

Query Match 29 3%; Score 478; DB 20; Length 312;
 Best Local Similarity 36 3%; Pred. No. 6.9e-31; Matches 110; Conservative 62; Mismatches 109; Indels 22; Gaps 8; DB 1 marrsrrh1-----lllrrlyvalgkayoiuskkdqyvtaveygeailac-k 51

Qy 3 LSRRLRLYARLRFHFLLFRGMI---EAVNLU:SNRNPVH-EFESVELSCII 55
 Db 56 THSOSDPRIEKKIQDGOTTYVFDNKIQGDLAGKTVGKSLRWNVTSRDSAIRC 115
 Db 52 tppkkvssrliekwkl-grsvsfyyqqtqgdfkraemi-dfnirknvtv:sdagkyrc 109

Qy 116 EVVALNDR KEVDEITIELIVOKPVKPVCRIPAAVPGKTAQLOQESEGYPRPHSWY 174
 Db 110 evsaspeqqnleedtvtievavapavpcvpsalsgtvtvelrcqdkgepiapaytwf 169

Qy 175 RNDVPLUTPSRANRFEQNSFFHVNSETGFLVNAVKHDQSGQYCIAASNDAGARCEOD 234
 Db 170 kdgiirlieprlqsgstqntskntqkqfntvsktscearnsngvhrccpkrmqdr 229

Qy 235 MEVDLNLIGIGGLVLLVAVITMGICCAVRRGCFTISKQDGESYKSPGKHGD 281
 Db 230 mqvdalnsgiaavvvvalvisvcgllcyaqrkgf-ssktsfqksnsskattmsen 289

Qy 292 NYI 294

DB 290 qwl 292

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GenCore version 4.5

Om protein - protein search, using sw model

Run on: August 6, 2001, 09:31:29 ; Search time 25.41 Seconds
(without alignments)
929.324 Million cell updates/sec

Title: US-09-524-531a-13

Perfect score: 1633

Sequence: 1 MALSRRRLRLYARLPHFLL.....VNVIRTSEBEGDFRKSSFVI 310

Scoring table: BLOSUM62

Gap open 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR:68:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

* Query Match Length DB ID

Result No. Score Match Length DB ID Description

Result No.	Score	Query	Match	Length	DB ID	Description
1	181	11.1	725	2	JE0099	neural cell adhesion molecule 1 - African clawed frog
2	180	11.0	1088	1	IUXNL	N: Alternative names: NCAM 1
3	178	10.9	1051	2	A39712	C: Species: Xenopus laevis (African clawed frog)
4	177	10.8	333	2	A31923	C: Date: 19-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
5	172.5	10.6	858	1	IURNC	C: Accession: JE0099
6	169.5	10.4	1115	1	IJMSNL	R; Kudo, M.; Takayama, E.; Tadakuma, T.; Shiokawa, K.
7	169	10.3	725	2	JE0100	Biochem. Biophys. Res. Commun. 245, 127-132, 1998
8	169	10.3	1092	1	JN0635	A: Title: Molecular cloning of ssd-form neural cell adhesion molecules (N-CAMs) as the
9	167.5	10.3	3707	2	SL0252	A: Reference number: JE0099; MUID:98204770
10	167.5	10.3	6042	2	T29157	A: Molecule type: mRNA
11	166	10.2	483	2	T17346	A: Residues: 1-725 <KUD>
12	166	10.2	483	2	T17346	A: Cross-references: DDBJ:AB008162; NID:93116226; PDB:BA25931.1; PID:93116227
13	164.5	10.1	352	2	T33433	C: Experimental source: heart
14	164.5	10.1	853	1	IURONC	C: Comment: This protein mediates and regulates various cell-cell interactions through
15	164	10.0	7962	2	T33346	C: Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; 1
16	163	10.0	761	1	IUJUNG	F:413-475/Domain: immunoglobulin homology <IMM>
17	162	9.9	5175	2	T0992	F:512-589/Domain: fibronectin type III repeat homology <3FR>
18	160	9.8	5198	2	T43290	
19	159.5	9.8	875	2	T33434	
20	159.5	9.8	1277	2	T0532	
21	157	9.6	1091	1	IRCHNL	
22	156	9.6	344	2	I55551	
23	156	9.6	1323	2	PNU568	
24	156	9.6	4162	2	T2633	
25	154.5	9.5	272	2	I49268	
26	153.5	9.4	1033	2	S19247	
27	153	9.4	1273	2	T42405	
28	152	9.3	538	2	JC3457	
29	151.5	811	2	A41054		

RESULT 1

JE0099

neural cell adhesion molecule 1 - African clawed frog

N: Alternative names: NCAM 1

C: Species: Xenopus laevis (African clawed frog)

C: Date: 19-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000

R; Kudo, M.; Takayama, E.; Tadakuma, T.; Shiokawa, K.

Biochem. Biophys. Res. Commun. 245, 127-132, 1998

A: Title: Molecular cloning of ssd-form neural cell adhesion molecules (N-CAMs) as the

A: Reference number: JE0099

A: Molecule type: mRNA

A: Residues: 1-725 <KUD>

A: Cross-references: DDBJ:AB008162; NID:93116226; PDB:BA25931.1; PID:93116227

C: Experimental source: heart

C: Comment: This protein mediates and regulates various cell-cell interactions through

C: Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; 1

F:413-475/Domain: immunoglobulin homology <IMM>

F:512-589/Domain: fibronectin type III repeat homology <3FR>

ALIGNMENTS

RESULT 2

IXNL

neural cell adhesion molecule long domain form precursor - African clawed frog

N: Alternative names: NCAM-180

N: Contains: neural cell adhesion molecule, short domain form (NCAM-140)

C: Species: Xenopus laevis (African clawed frog)

C: Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 22-Jun-1999

C: Accession: S09600

R; Krieg, P.A.; Sakaguchi, D.S.; Kinther, C.R.

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OM protein - protein search, using sw model

Run on:

August 6, 2001, 09:33:40 ; Search time 13.3 Seconds

Sequence:

US-09-524-531A-13
1 MAISRRRLRLYARLPHFPL.....VNYIRTSEEGDFRHKKSSFVI 310

Title:

Perfect score: 1633

Scoring table:

BLOSUM62

Sequence:

Gapop 10.0 , Gapext 0.5

Scored:

93435 seqs, 34255486 residues

Top number of hits satisfying chosen parameters:

93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing:

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	505	30.9	298	1 VEGA_HUMAN	P57087 homo sapien
2	449.5	27.5	300	1 JAM1_MOUSE	088792 mus musculus
3	415	25.4	299	1 JAM1_BOVIN	098624 homo sapien
4	409.5	25.1	298	1 JAM1_BOVIN	098750 bos taurus
5	242.5	14.8	319	1 A333_HUMAN	099795 homo sapien
6	180	11.0	1088	1 NCAL_XENLA	P16170 xenopus laevis
7	178	10.9	1051	1 PTK7_CHICK	091048 gallus gallus
8	177	10.8	333	1 AMAIL_DRONE	P15364 drosophila
9	172.5	10.6	365	1 CXAR_HUMAN	P78310 homo sapien
10	172.5	10.6	837	1 NCAL2_MOUSE	035136 mus musculus
11	172.5	10.6	658	1 NCAL1_RAT	P13596 rattus norvegicus
12	170	10.4	349	1 LACH_SCHRAM	P026474 schistocerca
13	169.5	10.4	115	1 NCAL2_MOUSE	P13594 mus musculus
14	169.5	10.4	1115	1 NCAL1_MOUSE	P13595 mus musculus
15	169	10.3	1092	1 NCAL2_XENLA	P36335 xenopus laevis
16	167.5	10.3	837	1 NCAL2_HUMAN	015394 homo sapien
17	167.5	10.3	3707	1 PGKBL_MOUSE	Q05793 mus musculus
18	164.5	10.1	853	1 NCAL1_BOVIN	P31836 bos taurus
19	163	10.0	761	1 NCAL2_HUMAN	P13592 homo sapien
20	163	10.0	848	1 NCAL1_HUMAN	P13591 homo sapien
21	161	9.9	1377	1 NCAL1_RAT	P97603 rattus norvegicus
22	159	9.7	1091	1 NCAL1_CHICK	P13590 gallus gallus
23	156	9.6	344	1 NTTR1_RAT	Q62718 rattus norvegicus
24	156	9.6	1493	1 NEOL_MOUSE	P97798 mus musculus
25	155	9.5	353	1 PCKL_CHICK	090773 gallus gallus
26	151.5	9.3	365	1 CXAR_MOUSE	P97792 mus musculus
27	151.5	9.3	811	1 FS21_DRONE	P34083 drosophila
28	151	9.3	873	1 FS21_DRONE	P34082 drosophila
29	151	9.2	1912	1 PTPD_HUMAN	P23468 homo sapien
30	150	9.2	1694	1 SN_MOUSE	Q62230 mus musculus
31	149.5	9.2	4393	1 PGKBL_HUMAN	P98160 homo sapien
32	148.5	9.1	1070	1 PTK7_HUMAN	Q13308 homo sapien
33	148.5	9.1	1461	1 NEOL_HUMAN	Q92859 homo sapien

RESULT	1	VEJA_HUMAN	STANDARD;	PRT;	298 AA.	ALIGNMENTS
RT		ID: VEJA_HUMAN				
RL		AC: PS7087;				
CC		DT: 01-OCT-2000 (Rel. 40, Created)				
CC		DT: 01-OCT-2000 (Rel. 40, Last sequence update)				
CC		DT: 01-OCT-2000 (Rel. 40, Last annotation update)				
DE		VASCULAR ENDOTHELIAL JUNCTION-ASSOCIATED MOLECULE PRECURSOR (VE-JAM).				
GN		C21ORF43.				
OS		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OC						
OX		NCBI_TAXID:9606;				
RN		[1]				
RP		SEQUENCE FROM N.A.				
RC		TISSUE:Vascular endothelial cells;				
RA		Palmer D., van Zante A., Huang C.C., Hemmerich S., Rosen S.-D.; 'Vascular endothelial junction-associated molecule, a novel member of the immunoglobulin superfamily, is localized to intercellular boundaries of endothelial cells.', J. Biol. Chem. 275:19139-19145(2000).				
RA		PMID:20317114; PubMed:1079521;				
RT		'Vascular endothelial junction-associated molecule, a novel member of the immunoglobulin superfamily, is localized to intercellular boundaries of endothelial cells.'				
RL		-I- FUNCTION: MAY PLAY A ROLE IN THE PROCESSES OF LYMPHOCYTE HOMING TO SECONDARY LYMPHOID ORGANS.				
CC		-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).				
CC		-I- TISSUE SPECIFICITY: PROMINENTLY EXPRESSED ON HIGH ENDOTHELIAL VENULES. IS ALSO PRESENT ON THE ENDOTHELIA OF OTHER VESSELS.				
CC		LOCALIZED TO THE INTERCELLULAR BOUNDARIES OF HIGH ENDOTHELIAL CELLS.				
CC		-I- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.				
CC		-I- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.				
CC		CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).				
CC		CC EMBL: AF255910; AAF81223; 1; -.				
DR		IMMUNOGLOBULIN domain; Glycoprotein; Transmembrane; Signal.				
KW		EMBL: AF255910; AAF81223; 1; -.				
FT		IMMUNOGLOBULIN domain; Glycoprotein; Transmembrane; Signal.				
FT		SIGNAL	1	20	POTENTIAL.	
FT		CHAIN	21	298		
FT		MOLECULE.				
FT		EXTRACELLULAR (POTENTIAL).				
FT		POTENTIAL.				
FT		CYTOSMERIC (POTENTIAL).				
FT		IG-LIKE V-TYPE DOMAIN.				
FT		IG-LIKE C2-TYPE DOMAIN.				
FT		POTENTIAL.				
FT		POTENTIAL.				
FT		N-LINKED (GlcNAc, -)				
FT		N-LINKED (GlcNAc, -)				
FT		N-LINKED (GlcNAc, -)				
SQ		SEQUENCE	298	AA:	33207 MW:	CA788518B2DCABE CRC64;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 6, 2001, 09:31:09 ; Search time 19.31 Seconds

Sequence: (without alignments)
330.554 Million cell updates/sec

Title: US-09-524-531a-13

Perfect score: 1633

Sequence: 1 MALSRRLRLYVARYLPHFLL.....VNVIRTSEBGDFRHKKSSFVI 310

Scoring table: BLOSUM62

Gapext 10.0 , Gapext 0.5

Searched: 197339 seqs, 2059346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*

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2: /cgn2_6/ptodata/1/iaa/5B_COMB_pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB_pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB_pep:*

5: /cgn2_6/ptodata/1/iaa/PCUTS_COMB_pep:*

6: /cgn2_5/ptodata/1/iaa/backtfilest.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	415	25.4	299	4	US-09-188-930-331	Sequence 331, APP
2	403	24.7	299	4	US-09-188-930-189	Sequence 189, APP
3	242.5	14.8	319	1	US-09-188-930-22	Sequence 22, APP
4	173.5	10.6	365	4	US-08-938-383B-2	Sequence 2, APP
5	172.5	10.6	365	2	US-08-919-424-3	Sequence 3, APP
6	172.5	10.6	365	4	US-08-922-426-2	Sequence 2, APP
7	171.5	10.5	2	US-08-979-424-1	Sequence 1, APP	
8	166	10.2	1101	3	US-08-986-485-2	Sequence 2, APP
9	160	9.8	869	1	US-08-374-834-16	Sequence 16, APP
10	160	9.8	869	2	US-08-921-712-29	Sequence 17, APP
11	156.5	9.6	365	4	US-08-920-383B-23	Sequence 23, APP
12	156.5	9.6	365	4	US-08-928-383B-24	Sequence 24, APP
13	151.5	9.3	4	US-08-928-383B-26	Sequence 25, APP	
14	151	9.2	1091	3	US-08-986-485-5	Sequence 5, APP
15	148	9.1	607	2	US-08-752-307B-12	Sequence 12, APP
16	147.5	9.0	501	2	US-08-905-31	Sequence 31, APP
17	147	9.0	95	4	US-08-928-383B-18	Sequence 18, APP
18	146.5	9.0	478	5	PCT-US93-08493-15	Sequence 15, APP
19	146.5	9.0	5	PCT-US93-08493-19	Sequence 19, APP	
20	146.5	9.0	868	5	PCT-US95-08493-21	Sequence 5, APP
21	144.5	8.8	698	2	US-08-602-725-36	Sequence 36, APP
22	144.5	8.8	734	2	US-08-899-429A-17	Sequence 17, APP
23	144.5	8.8	734	3	US-08-987-862A-17	Sequence 17, APP
24	144.5	8.8	868	1	PCT-US93-08493-1	Sequence 1, APP
25	144.5	8.8	868	2	US-08-644-271-1	Sequence 1, APP
26	141	8.6	338	2	US-08-414-657D-60	Sequence 60, APP
27	141	8.6	1	US-08-217-299-1	Sequence 1, APP	

RESULT 1

US-09-188-930-331

; Sequence 331, Application US/09188930A

; Patent No. 6150502

; GENERAL INFORMATION:

; APPLICANT: Watson, James D.

; APPLICANT: Strachan, Lorna

; APPLICANT: Sleeman, Matthew

; APPLICANT: Onrust, René

; APPLICANT: Murison, James Greg

; TITLE OF INVENTION: Compositions Isolated From Skin Cells

; FILE REFERENCE: 11000.101C1

; CURRENT APPLICATION NUMBER: US/09/188,930A

; CURRENT FILING DATE: 1988-11-09

; NUMBER OF SEQ ID NOS: 348

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 331

; LENGTH: 299

; TYPE: PRT

; ORGANISM: Human

; US-09-188-930-331

ALIGNMENTS

Sequence 3, APP1

Sequence 3, APP1

Sequence 11, APP1

Sequence 25, APP1

Sequence 2, APP1

Sequence 45, APP1

Sequence 42, APP1

Sequence 43, APP1

Sequence 56, APP1

Sequence 57, APP1

Sequence 49, APP1

Sequence 44, APP1

Sequence 45, APP1

Sequence 47, APP1

Sequence 2, APP1

Sequence 41, APP1

Sequence 7, APP1

US-09-188-930-189
; Sequence No. 189, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, René
; TITLE OF INVENTION: Compositions Isolated From Skin Cells and Methods For Their Use
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 189
; LENGTH: 299
; TYPE: PRT
; 3ANISM: Human
; NAME/KEY: UNSURE
; LOCATION: (247)...(247)
; ME/KEY: UNSURE
; LOCATION: (289)...(289)
; US-09-188-930-189

Query Match 24.7%; Score 403; DB 4; Length 299;
Best Local Similarity 33.1%; Pred. No. 1.2e-32;
Matches 98; Conservative 50; Mismatches 134; Indels 14; Gaps 6;
Qy 18 FFLFLLFLFRGCMIEAVNLKSSNRNPVHREFESVELLSCTITHSQTSDSPRIENKKIQPGQTY 77
Db 15 FILAALICSLALGSLGVHSSEPERIPENPVKSLC-AVSGFSSPRVNEFKDQDTTRL 72
Qy 78 VYFDNIKIOGLADGRDFVGKSLRWNVNTSDAATYCEVALNDRKEVDITILIVQV 137
Db 73 VCYNNIKITASVEDRY-TFLPQGTRKSVTWRDTGTYTC-MVSEEGGNSYGEVKVVLIVL 130
Qy 138 KPVPTVCRIPRAVPGKTANLQCOSEGYPRPHYSWYRNQVPLPDSRAMPFQNSFH 197
Db 131 PPSKPKPVNIPSSATIGNRATVTCSPQDGSPSEYTFKDGIVMPTNPKSTRAFNSHSSYVL 190
Qy 198 NSET3LVLVNAVKHDQSGQYCTIASNDAGARCEQ-DMEYDNLNTAGITGGVLVVLIVL 256
Db 191 NPTTGTSLVFDPLSACDTGEYCEARINGYGPMTSNAVRMEAVRNQVIVAVLWYXILL 250
Qy 257 AVITMGICCAVRRGPFISSKQDGEEYKSPGKHGDGYNIVRS--EEDDERIKSSFYI 310
Db 251 GILVFGIWFAYSRGHDRTKGTSRK-----VIYSQPSARSKXEFKOTSSFLV 299
Db 294 BREEEDDYRQE 304
RESULT 3
US-08-597-495B-22
; Sequence 22, Application US/08597495B
; Patent No. 512369
; GENERAL INFORMATION:
; APPLICANT: Old, Lloyd J.; Welt, Sydney; Ritter, Gerd;
; APPLICANT: Simpson, Richard J.; Nice, Édouard; Moritz, R. L.;
; APPLICANT: Cattinel, B.; Ji, Hong; Burgess, Anthony W.;
; APPLICANT: Heath, Joan K.; White, Sara J.; Johnstone, Cameron
; TITLE OF INVENTION: Colon Cell And Colon Cancer Cell
; TITLE OF INVENTION: Associated Nucleic Acid Molecules, Protein And Peptides
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:

RESULT 4
US-08-928-383B-2
; Sequence 2, Application US/08928383B
; Patent No. 6210921
; GENERAL INFORMATION:
; APPLICANT: Robert W. Fibberg, Jeffrey M. Bergelson,
; APPLICANT: and Marshall S. Horwitz
; TITLE OF INVENTION: CAR, A NO. 6210921el Coxsackievirus and Adenovirus
; TITLE OF INVENTION: Receptor
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM: